

32	320.5	19.9	343	1	GP81_MOUSE	O8c131 mus musculu
33	320.5	19.9	361	1	P2Y4_RAT	O35811 rattus norv
34	319	19.8	328	1	P2Y6_RAT	O63371 rattus norv
35	319	19.8	373	1	P2Y2_MOUSE	F35383 mus musculu
36	318	19.7	362	1	P2YR_CHICK	P34996 gallus gall
37	318	19.7	362	1	P2YR_MELGA	P49652 meleagris g
38	318	19.7	374	2	O57466	O57466 meleagris g
39	317.5	19.7	346	1	CLT2_HUMAN	O9ns75 homo sapien
40	317	19.6	309	1	CLT2_RAT	O324t9 rattus norv
41	315.5	19.5	361	1	P2Y4_MOUSE	Q3jj87 mus musculu
42	315.5	19.5	365	1	P2Y4_HUMAN	P51582 homo sapien
43	315.5	19.5	396	1	BRB2_RAT	P25023 rattus norv
44	312.5	19.4	364	2	Q68DN6	Q68dm8 homo sapien
45	312.5	19.4	391	1	BRB2_HUMAN	P30411 homo sapien

## ALIGNMENTS

RESULT 1  
GP35\_HUMAN  
ID GP35\_HUMAN STANDARD; PRT; 309 AA.  
AC Q9HC97; O43495; Q86UH4;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Probable G protein-coupled receptor GPR35.  
DE Name=GPR35; (Human)  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98140132; PubMed=9479505; DOI=10.1006/geno.1998.5095;  
RA O'Dowd B.F., Nguyen T., Marchese A., Cheng R., Lynch K.R.,  
RA Heng H.H.Q., Kolakowski L.F. Jr., George S.R.;  
RT "Discovery of three novel G-protein-coupled receptor genes.";  
RL Genomics 47:310-313(1998)  
RN [2]  
RP SEQUENCE FROM N.A., AND VARIANTS THR-25; ILE-29; MET-108; SER-125;  
RP MET-253 AND SER-294.  
RX MEDLINE=20472315; PubMed=11017071; DOI=10.1038/79876;  
RA Horikawa Y., Oda N., Cox N.J., Li X., Orho-Melander M., Hara M.,  
RA Hinokio Y., Lindner T.H., Mashima H., Schwarz P.E.H.,  
RA del Bosque-Plata L., Horikawa Y., Oda Y., Yoshiuchi I., Colilla S.,  
RA Polonsky K.S., Wei S., Concannon P., Iwasaki N., Schulze J.,  
RA Baier L.J., Bogardus C., Groop L., Boerwinkle E., Hanis C.L.,  
RA Bell G.I.;  
RT "Genetic variation in the gene encoding calpain-10 is associated with  
RT type 2 diabetes mellitus";  
RL Nat. Genet. 26:163-175(2000).  
RN [3]  
RP SEQUENCE FROM N.A., AND VARIANT SER-294.  
RA Warren C.N., Aronstam R.S., Sharma S.V.;  
RT "cDNA clones of human proteins involved in signal transduction  
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";  
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Orphan receptor.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -!- TISSUE SPECIFICITY: Expressed in all adult and fetal tissues  
CC examined, including pancreatic islets and skeletal muscle, with  
CC relatively higher levels in adult lung, small intestine, colon and  
CC stomach.  
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

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CC EMBL; AF027957; AAC52028.1; --
DR EMBL; AF089087; AAG17965.1; --
DR EMBL; AY275467; AAB32299.1; --
DR GenBank; HGNC:4492; GPR35.
DR MIM; 602646; --
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.
DR PROSITE; PS0262; G PROTEIN RECEPTOR FL2; 1.
KW G-protein coupled receptor; Glycoprotein; Polymorphism; Transmembrane.
FT DOMAIN 1 24
FT TRANSMEM 25 45
FT DOMAIN 46 56
FT TRANSMEM 57 77
FT DOMAIN 78 90
FT TRANSMEM 91 112
FT DOMAIN 113 135
FT TRANSMEM 136 156
FT DOMAIN 157 174
FT TRANSMEM 175 195
FT DOMAIN 196 218
FT TRANSMEM 219 239
FT DOMAIN 240 258
FT TRANSMEM 259 279
FT DOMAIN 280 309
FT DISULFID 89 162
FT CARBOHYD 2 2
FT VARIANT 25 25
FT VARIANT 29 29
FT VARIANT 108 108
FT VARIANT 125 125
FT VARIANT 253 253
FT VARIANT 294 294
FT CONFLICT 174 174 A -> R (in Ref. 1).
FT SEQUENCE 309 AA; 34141 MW; FC034FB7231B26F1 CRC64;

Query Match 99.6%; Score 1608; DB 1; Length 309;
Best Local Similarity 99.7%; Pred. No. 7.5e-114;
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTPWPAIKLGFYAYLVGLVLLVGLLNSLALWVFCRMOQWTEIRYMT 60
Db 1 MNGTYNTCGSSDLTPWPAIKLGFYAYLVGLVLLVGLLNSLALWVFCRMOQWTEIRYMT 60
QY 61 NLAVADLCLLCTLPFVLSLRDTSPTPLCOLSGIYLTNRNMSISLVTAIAVDRYAVRH 120
Db 61 NLAVADLCLLCTLPFVLSLRDTSPTPLCOLSGIYLTNRNMSISLVTAIAVDRYAVRH 120
QY 121 PLRARGLRSPQAAAVCAVLWLVIGSLVARWLLGIQGGFCFRSTRHFNFSNRPFLG 180
Db 121 PLRARGLRSPQAAAVCAVLWLVIGSLVARWLLGIQGGFCFRSTRHFNFSNRPFLG 180
QY 181 YLPLAVVVFCSLKVVTALAQRPPTDVQGAETRAKAAVMWVANLLVFVCFPLPHVGLTVR 240
Db 181 YLPLAVVVFCSLKVVTALAQRPPTDVQGAETRAKAAVMWVANLLVFVCFPLPHVGLTVR 240
QY 241 LAVGNACALLETIRRALYITSKLSDANCCCLDAICYYTMAKEFQESALAVAPRAKAHKS 300
Db 241 LAVGNACALLETIRRALYITSKLSDANCCCLDAICYYTMAKEFQESALAVAPRAKAHKS 300
QY 301 QDSLCTVTLA 309
Db 301 QDSLCTVTLA 309

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RESULT 2
Q6ZMP9
ID O6ZMP9 PRELIMINARY; PRT; 394 AA.
AC O6ZMP9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein FLJ16773.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RA Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AK131540; RAD18676.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPS.
DR PROSITE; PS00237; G PROTEIN RECEPTOR FL1; 1.
DR PROSITE; PS0262; G PROTEIN RECEPTOR FL2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 394 AA; 43308 MW; 1598FD4BAE4233C CRC64;

Query Match 99.3%; Score 1602; DB 2; Length 394;
Best Local Similarity 99.4%; Pred. No. 2.6e-113;
Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTPWPAIKLGFYAYLVGLVLLVGLLNSLALWVFCRMOQWTEIRYMT 60
Db 86 MNGTYNTCGSSDLTPWPAIKLGFYAYLVGLVLLVGLLNSLALWVFCRMOQWTEIRYMT 145
QY 61 NLAVADLCLLCTLPFVLSLRDTSPTPLCOLSGIYLTNRNMSISLVTAIAVDRYAVRH 120
Db 146 NLAVADLCLLCTLPFVLSLRDTSPTPLCOLSGIYLTNRNMSISLVTAIAVDRYAVRH 205
QY 121 PLRARGLRSPQAAAVCAVLWLVIGSLVARWLLGIQGGFCFRSTRHFNFSNRPFLG 180
Db 206 PLRARGLRSPQAAAVCAVLWLVIGSLVARWLLGIQGGFCFRSTRHFNFSNRPFLG 265
QY 181 YLPLAVVVFCSLKVVTALAQRPPTDVQGAETRAKAAVMWVANLLVFVCFPLPHVGLTVR 240
Db 266 YLPLAVVVFCSLKVVTALAQRPPTDVQGAETRAKAAVMWVANLLVFVCFPLPHVGLTVR 325
QY 241 LAVGNACALLETIRRALYITSKLSDANCCCLDAICYYTMAKEFQESALAVAPRAKAHKS 300
Db 326 LAVGNACALLETIRRALYITSKLSDANCCCLDAICYYTMAKEFQESALAVAPRAKAHKS 385
QY 301 QDSLCTVTLA 309
Db 386 QDSLCTVTLA 394

RESULT 3
GP35_MOUSE
ID GP35_MOUSE STANDARD; PRT; 307 AA.
AC Q9ES90;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)

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28	87.8	9.4	2582	3	US-08-944-496-6	Sequence 6, Appli
29	87.8	9.4	2582	3	US-08-925-767-6	Sequence 6, Appli
30	87.4	9.4	1077	4	US-09-170-496D-39	Sequence 39, Appl
31	87.4	9.4	1077	4	US-09-170-496D-185	Sequence 185, App
32	86	9.2	1113	4	US-09-826-509-540	Sequence 540, App
33	86	9.2	1805	3	US-08-405-271A-18	Sequence 18, Appl
34	86	9.2	1373	4	US-09-016-434-1391	Sequence 1391, Ap
35	86	9.2	1373	4	US-09-023-655-1417	Sequence 1417, Ap
36	86	9.2	3205	4	US-09-976-594-171	Sequence 171, App
37	85.6	9.2	2025	4	US-09-016-434-1482	Sequence 1482, Ap
38	85.6	9.2	2025	4	US-09-814-915A-74	Sequence 74, Appl
39	82.4	8.9	1842	1	US-08-442-134A-1	Sequence 1, Appli
40	82.4	8.9	1842	1	US-08-444-581B-1	Sequence 1, Appli
41	82.4	8.9	1842	1	US-08-446-088A-1	Sequence 1, Appli
42	81	8.7	1594	2	US-08-955-713-1	Sequence 1, Appli
43	80.6	8.7	1059	3	US-09-576-160B-9	Sequence 9, Appli
44	79	8.5	1059	3	US-09-576-160B-8	Sequence 8, Appli
45	79	8.5	1285	4	US-09-016-434-1366	Sequence 1366, Ap

## ALIGNMENTS

RESULT 1  
US-09-422-869-21  
; Sequence 21, Application US/09422869  
; Patent No. 6235481  
; GENERAL INFORMATION:  
; APPLICANT: POLONSKY, KENNETH S.  
; APPLICANT: HORIKAWA, YUKIO  
; APPLICANT: ODA, NAOHISA  
; APPLICANT: COX, NANCY J.  
; APPLICANT: SEENAN, SEAMUS  
; APPLICANT: ZHOU, YUN-PING  
; APPLICANT: OTANI, KENICHI  
; APPLICANT: HANIS, CRAIG I.  
; APPLICANT: BELL, GRAEME I.  
; TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES  
; FILE REFERENCE: ARCD:307  
; CURRENT APPLICATION NUMBER: US/09/422,869  
; CURRENT FILING DATE: 1999-10-21  
; EARLIER APPLICATION NUMBER: 60/134,175  
; EARLIER FILING DATE: 1999-05-13  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 1875  
; TYPE: DNA  
; ORGANISM: Human  
US-09-422-869-21

Query Match 99.0%; Score 920.4; DB 3; Length 1875;  
Best Local Similarity 99.4%; Pred. No. 6.5e-197;  
Matches 924; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY	1	ATGATGGCACCCTACAAACACCTGTGGCTCCAGGACCTCACCTGGCCCCCAGCGATCAAG	60
Db	576	ATGATGGCACCCTACAAACACCTGTGGCTCCAGGACCTCACCTGGCCCCCAGCGATCAAG	635
QY	61	CTGGGCTTCTACGCCCTACCTTGGCGCTCTGTGGTGTAGGCTGTCTCAACAGCCTG	120
Db	636	CTGGGCTTCTACGCCCTACCTTGGCGCTCTGTGGTGTAGGCTGTCTCAACAGCCTG	695
QY	121	GGGCTCTGGGTGTCTGTGGCGCATGAGGAGTGGAGACCGGATCTACATGACC	180
Db	696	GGGCTCTGGGTGTCTGTGGCGCATGAGGAGTGGAGACCGGATCTACATGACC	755
QY	181	AACCTGGCGGTGGCGACCTCTGCTGTGTGACCTTGCCTTGTGTGTGACTCCCTG	240
Db	756	AACCTGGCGGTGGCGACCTCTGCTGTGTGACCTTGCCTTGTGTGTGACTCCCTG	815
QY	241	CGAGACACCTCAGACACGCGCTGTGCCAGCTCTCCAGGGATCTTACCTGACCAACAGG	300

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816	CGAGACACCTCAGACACGCCCGCTGTGCCAGCTCTCCAGGGCATCTACCTGACCAACAGG	875
301	TACATGAGCATCAGCCTGGTTCACGGCCATCCCGCTGAGACCGCTATATGGCCGTCGCGCAC	360
876	TACATGAGCATCAGCCTGGTTCACGGCCATCCCGCTGAGACCGCTATATGGCCGTCGCGCAC	935
361	CGCCTCGGTCCCGCGGGCTGCCGTCCCCAGAGCAGCTGCGGCGGTGTCGCGGTCTTC	420
936	CGCCTCGGTCCCGCGGGCTGCCGTCCCCAGAGCAGCTGCGGCGGTGTCGCGGTCTTC	995
421	TGGGTGCTTGGTTCATCGCTCCCTCGTGGTTCGCTGGTCTCTTGGGGATTTCAGGAGGGCGGC	480
996	TGGGTGCTTGGTTCATCGCTCCCTCGTGGTTCGCTGGTCTCTTGGGGATTTCAGGAGGGCGGC	1055
481	TTCTGCTTCAGGAGCACCGGCAAAATTTCAAATCCATGCGGTTCCCGCTGCTGGGATTTC	540
1056	TTCTGCTTCAGGAGCACCGGCAAAATTTCAAATCCATGCGGTTCCCGCTGCTGGGATTTC	1115
541	TACCTGCCCTCGGCCGTGGTGGTCTTCTGTCTCCCTGAAGTGGTGAATGCCCTGGGCCAG	600
1116	TACCTGCCCTCGGCCGTGGTGGTCTTCTGTCTCCCTGAAGTGGTGAATGCCCTGGGCCAG	1175
601	AGGCACCCACCGACGTGGGGCAGGACAGGGCCACCCGCGAAGGCTAAACGATGGTCTGG	660
1176	AGGCACCCACCGACGTGGGGCAGGACAGGGCCACCCGCGAAGGCTGGCCGATGGTCTGG	1235
661	GCCAACTCTGTGTGTTGTTGGTGTCTGTTCTCTGCCCTGCACGTGGGGCTGACAGTGGCG	720
1236	GCCAACTCTGTGTGTTGTTGGTGTCTGTTCTCTGCCCTGCACGTGGGGCTGACAGTGGCG	1295
721	CTCGCAGTGGGCTGGAAACGCTGTGCCCTCTCTGGAGACGATCCGTGCGGCCCTGTATATA	780
1296	CTCGCAGTGGGCTGGAAACGCTGTGCCCTCTCTGGAGACGATCCGTGCGGCCCTGTATATA	1355
781	ACCAGCAGCTCTCAGATGCCAACTGCTGCTGGACCGCATCTGCTACTACTACTACATGGCC	840
1356	ACCAGCAGCTCTCAGATGCCAACTGCTGCTGGACCGCATCTGCTACTACTACTACATGGCC	1415
841	AAGGAGTTTCAGAGGGGCTCTGCACCTGGCCGTGGCTCCCGGTGCTAAGGCCCAACAAAGC	900
1416	AAGGAGTTTCAGAGGGGCTCTGCACCTGGCCGTGGCTCCCGGTGCTAAGGCCCAACAAAGC	1475
901	CAGGACTCTCTGTGGGTGACCTCGCCATAA	930
1476	CAGGACTCTCTGTGGGTGACCTCGCCATAA	1505

## RESULT 2

```

US-09-422-869-1
; Sequence 1, Application US/09422869
; Patent No. 6235481
; GENERAL INFORMATION:
; APPLICANT: POLONSKY, KENNETH S.
; APPLICANT: HORIKAWA, YUKIO
; APPLICANT: ODA, NAOHISA
; APPLICANT: COX, NANCY J.
; APPLICANT: SREENAN, SEAMUS
; APPLICANT: ZHOU, YUN-PING
; APPLICANT: OTANI, KENICHI
; APPLICANT: HANIS, CRAIG L.
; APPLICANT: BELL, GRAEME I.
; TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES
; FILE REFERENCE: ARCD:307
; CURRENT APPLICATION NUMBER: US/09/422,869
; CURRENT FILING DATE: 1999-10-21
; EARLIER APPLICATION NUMBER: 60/134,175
; EARLIER FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1

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Query Match 99.0%; Score 920.4; DB 3; Length 49136;  
 Best Local Similarity 99.4%; Pred. No. 1.3e-196;  
 Matches 924; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY	1	ATGAATGGCAGCTACAAACCTGTGGGTCCAGCGACCTCACCTGGGCCCCAGCGATCAAG	60
DB	43645	ATGAATGGCACTTACAAACCTGTGGGTCCAGCGACCTCACCTGGGCCCCAGCGATCAAG	43704
QY	61	CTGGGCTTCTAGCGCTACTTTGGGGCGTCTTGTGTGTGTAGGCGTGTCTCAACAGCGCTG	120
DB	43705	CTGGGCTTCTAGCGCTACTTTGGGGCGTCTTGTGTGTGTAGGCGTGTCTCAACAGCGCTG	43764
QY	121	GGGCTCTGGGTGTCTGTGTGGCGATGACAGATGGACGAGACCCGCGATCTACATGACC	180
DB	43765	GGGCTCTGGGTGTCTGTGTGGCGATGACAGATGGACGAGACCCGCGATCTACATGACC	43824
QY	181	AACCTGGGGGTGGCGACCTCTGCGCTGTGTGACACTTGGCCCTTGTGTGTGTGCTCCCTG	240
DB	43825	AACCTGGGGGTGGCGACCTCTGCGCTGTGTGACACTTGGCCCTTGTGTGTGTGCTCCCTG	43884
QY	241	CGAGACACTTACAGACGCGCGTGTGGCAGCTCTCCAGGCGCATCTACTGACCAACAGG	300
DB	43885	CGAGACACTTACAGACGCGCGTGTGGCAGCTCTCCAGGCGCATCTACTGACCAACAGG	43944
QY	301	TACATGAGCATCAGCTGTGTGACGCGCATCGCGGTGACCGGTATGTGGCGGTGCGGCAC	360
DB	43945	TACATGAGCATCAGCTGTGTGACGCGCATCGCGGTGACCGGTATGTGGCGGTGCGGCAC	44004
QY	361	CGGCTGCGTCCCGCGGGCTGCGGTCCCGCAGGCAAGGTGTGGCGCGTGTGGCGTCTC	420
DB	44005	CGGCTGCGTCCCGCGGGCTGCGGTCCCGCAGGCAAGGTGTGGCGCGTGTGGCGTCTC	44064
QY	421	TGGGTGCTGTGTATGGGCTTCCTGTGGTGTGCTGTGGCTCTGGGGATTCAGAGGGCGGC	480
DB	44065	TGGGTGCTGTGTATGGGCTTCCTGTGGTGTGCTGTGGCTCTGGGGATTCAGAGGGCGGC	44124
QY	481	TTCTGTCTTACGAGACACCGGCACAATTTCAACTCCATCGGTTCCCGTCTGGGATTC	540
DB	44125	TTCTGTCTTACGAGACACCGGCACAATTTCAACTCCATCGGTTCCCGTCTGGGATTC	44184
QY	541	TACTGCGCCCTGGCGGTGTGTCTTCTGCTCCCTGAAGTGGTGTACTGCCCTGGCCAG	600
DB	44185	TACTGCGCCCTGGCGGTGTGTCTTCTGCTCCCTGAAGTGGTGTACTGCCCTGGCCAG	44244
QY	601	AGGCGACCCACAGCTGGGGCAGGAGGAGGCGACCCGCAAGGCTTAAACGATGTCTGG	660
DB	44245	AGGCGACCCACAGCTGGGGCAGGAGGAGGCGACCCGCAAGGCTTAAACGATGTCTGG	44304
QY	661	GCCAACTCTGTGTGTGTGTCTGCTTCTGCGCCCTGCAGTGGGGGTGACGTGGGC	720
DB	44305	GCCAACTCTGTGTGTGTGTCTGCTTCTGCGCCCTGCAGTGGGGGTGACGTGGGC	44364
QY	721	CTGCGATGGGCTGGAAACGCTGTGGCCCTCTGGAGAGCATCCGTCGCGCCCTGTACATA	780
DB	44365	CTGCGATGGGCTGGAAACGCTGTGGCCCTCTGGAGAGCATCCGTCGCGCCCTGTACATA	44424
QY	781	ACAGCAAGCTCTCAGATGCAACTGCTGCTGGAGCGCATCTGCTACTACTACTAGGCC	840
DB	44425	ACAGCAAGCTCTCAGATGCAACTGCTGCTGGAGCGCATCTGCTACTACTACTAGGCC	44484
QY	841	AAGGAGTTCCAGAGGCGGTCTGCACTGGCGGTGTCTCCCGTGTCTAAGGCCCAAAAGC	900
DB	44485	AAGGAGTTCCAGAGGCGGTCTGCACTGGCGGTGTCTCCCGTGTCTAAGGCCCAAAAGC	44544
QY	901	CAGGACTCTGTGGCGTGAACCTTCGCTTAA	930
DB	44545	CAGGACTCTGTGGCGTGAACCTTCGCTTAA	44574

### RESULT 3

US-09-724-864-29

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28	308.5	19.1	375	4	US-09-947-922-3	Sequence 3, Appli
29	306	19.0	328	3	US-08-513-974B-39	Sequence 39, Appl
30	306	19.0	328	3	US-08-513-974B-371	Sequence 371, App
31	306	19.0	328	4	US-09-461-436B-39	Sequence 39, Appl
32	305.5	18.9	354	4	US-09-364-425B-60	Sequence 60, Appl
33	305.5	18.9	358	3	US-09-041-545-2	Sequence 2, Appli
34	305.5	18.9	358	3	US-09-327-925-2	Sequence 2, Appli
35	305.5	18.9	362	4	US-09-170-496D-4	Sequence 4, Appli
36	305	18.9	259	3	US-09-261-599B-3	Sequence 3, Appli
37	305	18.9	259	4	US-09-456-455A-3	Sequence 61, Appl
38	304.5	18.9	93	3	US-09-724-864-61	Sequence 186, App
39	304.5	18.9	358	4	US-09-170-496D-186	Sequence 2, Appli
40	304	18.8	342	4	US-09-054-272-2	Sequence 555, App
41	304	18.8	342	4	US-09-826-509-555	Sequence 39, Appl
42	303	18.8	326	1	US-08-118-270-39	Sequence 39, Appl
43	303	18.8	326	5	PCT-US93-08528-39	Sequence 4, Appli
44	302.5	18.7	373	2	US-08-559-524A-4	Sequence 4, Appli
45	302.5	18.7	373	3	US-08-749-707-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1  
 US-09-422-869-20  
 ; Sequence 20, Application US/09422869  
 ; Patent No. 6235481  
 ; GENERAL INFORMATION:  
 ; APPLICANT: POLONSKY, KENNETH S.  
 ; APPLICANT: HORIKAWA, YUKIO  
 ; APPLICANT: ODA, NAOHISA  
 ; APPLICANT: COX, NANCY J.  
 ; APPLICANT: SREENAN, SEAMUS.  
 ; APPLICANT: ZHOU, YUN-PING  
 ; APPLICANT: OTANI, KENICHI  
 ; APPLICANT: HANIS, CRAIG L.  
 ; APPLICANT: BELL, GRAEME I.  
 ; TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES  
 ; FILE REFERENCE: ARCD:307  
 ; CURRENT APPLICATION NUMBER: US/09/422,869  
 ; CURRENT FILING DATE: 1999-10-21  
 ; EARLIER APPLICATION NUMBER: 60/134,175  
 ; EARLIER FILING DATE: 1999-05-13  
 ; NUMBER OF SEQ ID NOS: 30  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 20  
 ; LENGTH: 309  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 US-09-422-869-20

Query Match	100.0%	Score 1614;	DB 3;	Length 309;
Best Local Similarity	100.0%	Pred. No. 7.1e-130;		
Matches 309;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

  

QY	1	MNGTYNTCGSSDLTWPPAIKLGFIAYLGVLVLLGLLNSLALWVFCRCMQWTETRIYNT	60
Db	1	MNGTYNTCGSSDLTWPPAIKLGFIAYLGVLVLLGLLNSLALWVFCRCMQWTETRIYNT	60
QY	61	NLAVALDCLLCTLPFVLSRLDTSPTPLCQLSQGIYLTNRNYSISLVTALAVDRYVAVRH	120
Db	61	NLAVALDCLLCTLPFVLSRLDTSPTPLCQLSQGIYLTNRNYSISLVTALAVDRYVAVRH	120
QY	121	PLRARGLSRQRAAACAVALWVLVIGSLVARWLLGIQGGFCFRSTRNFRNFRPPLGFG	180
Db	121	PLRARGLSRQRAAACAVALWVLVIGSLVARWLLGIQGGFCFRSTRNFRNFRPPLGFG	180
QY	181	YLPLAVVVFCSLKVVYTAQAQRPPTDVGQAEATRAARWVANLLVFVVCFLPHVGLTVR	240
Db	181	YLPLAVVVFCSLKVVYTAQAQRPPTDVGQAEATRAARWVANLLVFVVCFLPHVGLTVR	240
QY	241	LAUCWACALLETTRRALYITSKLSANDCCCLDAICYYYMAKEFQESALAVAPRAKAHKS	300

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Db 241 LAVGNACALLETIRRALYITSKLSDANCCDAICYYMAKEFOEASALAVAPRAKAHS 300  
QY 301 QDSLCVTLA 309  
Db 301 QDSLCVTLA 309

RESULT 2  
US-08-781-250-2  
; Sequence 2, Application US/08781250  
; Patent No. 6010877  
; GENERAL INFORMATION:  
; APPLICANT: Sathe, Ganesh  
; APPLICANT: Van Horn, Stephanie  
; APPLICANT: Bergsma, Derk  
; APPLICANT: Mao, Joyce Yue  
; TITLE OF INVENTION: CDNA CLONE H8CS41 THAT ENCODES A NOVEL 7-TRANSMEMBRAN  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/781,250  
; FILING DATE: 10-JAN-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: William T. Han,  
; REGISTRATION NUMBER: 34,344  
; REFERENCE/DOCKET NUMBER: ATGS0043  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5219  
; TELEFAX: 610-270-4060  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 370 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-781-250-2

Query Match 24.9%; Score 402; DB 3; Length 370;  
Best Local Similarity 34.1%; Pred. No. 1.3e-26;  
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AYVLGVLGLLNSLALWVFCRMOOWTETRIYMTNLAVADLCLCTLPF-VLHSLR-- 81  
Db 44 AVTSVFILGLIINVSLSLWFCRMRKSRSTAFITNLAVSDLLFVCTLPFKIFYFNH 103  
QY 82 -DTSDFPLCOLSQGIVLTNRYSISLVTAIADRYVAVRHPRLRARGLSRQAAAVCAVL 140  
Db 104 WPGDIT-LCKISGTAFLTNIYGSMLFCTISVDRLAIVYFPRSTIRTRNSAIVCAGV 162  
QY 141 WLVLGSLVARLLGQEG-----GGCFSTRHNFNSMR--FPLGLFYPLAVVVF 189  
Db 163 WILVLSGGISASLSTNNVNNATTCPEGFSKRWKTYLSKITIFIEVVGFIPLINVS 222  
QY 190 CSLKVVVTAQAQRPTDVGQAEAT-RKAARMVMANLAVFVVCFLPHVGLTVRLAVGNAC 248  
Db 223 CSSVVLRLT--RKPATLSQIGTKKKVKRLMTVHMAVFFVVCFFYNSVLFLYALVRSQAI 280

QY 249 --ALLETIRRALY-ITSKLSDANCCDAICYYMAKEFOEASALAVAPRAKAHSQDSLC 305  
Db 281 TNCFLERPAKIWPITLCLATLNCDFDFIYFTLESQKSFYI-----NAHIRMESLIF 334  
QY 306 VT 307  
Db 335 KT 336

## RESULT 3

US-09-170-496D-108  
; Sequence 108, Application US/09170496D  
; Patent No. 6555339  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Liaw, Chen W.  
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: AREN-0040  
; CURRENT APPLICATION NUMBER: US/09/170,496D  
; CURRENT FILING DATE: 1998-10-13  
; NUMBER OF SEQ ID NOS: 294  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 108  
; LENGTH: 387  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-170-496D-108

Query Match 22.8%; Score 368.5; DB 4; Length 387;  
Best Local Similarity 34.3%; Pred. No. 9.6e-24;  
Matches 95; Conservative 48; Mismatches 105; Indels 29; Gaps 11;

QY 27 LGVLVLGLLNSLALWVFCRMOOWTETRIYMTNLAVADLCLCTLPVL-----HSLR 81  
Db 34 LGLEFIPLGLLGLALWIFCPHLKSKWSRIPLFNLAADVADFLIILCLPPVMDYVYVRSOW 93  
QY 82 DTSDFPLCOLSQGIVLTNRYSISLVTAIADRYVAVRHPRLRARGLSRQAAAVCAVL 141  
Db 94 NFGDIP-CRLVLFMFAMNRQSGIIFLTVAVDYFRVVPHPHALNKISNWTAAIISCLLW 152  
QY 142 VLIVIG---SLVARMLLGIQEG--GCFER-STRHNF--NSMRPFLGFLYPLAVVVFCSLK 193  
Db 153 GITVGLTVHLLKKLL-LQNGPANVCISFSICHTFRWHEAMP-LLEFLPLGLIILFCSAR 210  
QY 194 VVTAQAQRPTDVGQAEATRKARMMWANLLVVFVVCFLPHVGLTVRLAVGW-----N 246  
Db 211 IIVSLRQR---QMDRHAKIKRAITFMVVAIVFVICFLP---SVVVRIRIFLLHTSGTQ 264  
QY 247 ACALLETIRRALYITSKLSDANCCDAICYYMAKEP 283  
Db 265 NCEVYSVDLAPFITLSFTYMSMLDPVVVYFSPSF 301

## RESULT 4

US-09-170-496D-222  
; Sequence 222, Application US/09170496D  
; Patent No. 6555339  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Liaw, Chen W.  
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: AREN-0040  
; CURRENT APPLICATION NUMBER: US/09/170,496D  
; CURRENT FILING DATE: 1998-10-13  
; NUMBER OF SEQ ID NOS: 294  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 222  
; LENGTH: 387

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 23, 2005, 11:17:30 ; Search time 19.5 Seconds  
(without alignments)  
1182.901 Million cell updates/sec

Title: US-10-083-168-16  
Perfect score: 1614  
Sequence: 1 MNGYNTCGSSDLTPWPAIK.....AVAPRAKAKSODSLCVTLA 309

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/1aa/5B COMB.pep:\*  
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4: /cgn2\_6/ptodata/1/1aa/6B COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCITUS COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	402	24.9	370	3	US-08-781-250-2
3	368.5	22.8	387	4	US-09-170-496D-108
4	368.5	22.8	387	4	US-09-170-496D-222
5	368.5	22.8	387	4	US-09-944-807-21
6	361.5	22.4	344	2	US-08-467-948A-8
7	361.5	22.4	344	2	US-08-467-947A-8
8	360.5	22.3	302	2	US-08-467-948A-30
9	360.5	22.3	302	3	US-08-467-947A-30
10	330.5	20.5	377	4	US-09-745-842-17
11	329.5	20.4	374	4	US-09-102-710B-3
12	321	19.9	362	3	US-08-513-974B-374
13	319.5	19.8	346	4	US-09-585-876-2
14	318	19.7	374	4	US-09-745-842-15
15	317	19.6	373	3	US-08-513-974B-373
16	315.5	19.5	365	4	US-09-745-842-16
17	315.5	19.5	365	4	US-09-077-173D-2
18	312.5	19.4	364	4	US-08-148-708-2
19	311.5	19.3	391	4	US-09-826-509-463
20	310.5	19.2	327	3	US-08-513-974B-372
21	310.5	19.2	362	4	US-09-170-496D-166
22	310	19.2	342	3	US-08-988-876-9
23	308.5	19.1	375	1	US-08-442-134A-2
24	308.5	19.1	375	1	US-08-444-581B-2
25	308.5	19.1	375	1	US-08-446-088A-2
26	308.5	19.1	375	2	US-08-559-524A-3
27	308.5	19.1	375	3	US-08-749-707-3

28 308.5 19.1 375 4 US-09-947-922-3 Sequence 3, Appli  
29 306 19.0 328 3 US-08-513-974B-39 Sequence 39, Appl  
30 306 19.0 328 3 US-08-513-974B-371 Sequence 371, App  
31 306 19.0 328 4 US-09-461-436B-39 Sequence 39, Appl  
32 305.5 18.9 354 4 US-09-364-425B-60 Sequence 60, Appl  
33 305.5 18.9 358 3 US-09-041-545-2 Sequence 2, Appli  
34 305.5 18.9 358 3 US-09-327-925-2 Sequence 2, Appli  
35 305.5 18.9 362 4 US-09-170-496D-4 Sequence 4, Appli  
36 305 18.9 259 3 US-09-261-599B-3 Sequence 3, Appli  
37 305 18.9 259 4 US-09-456-455A-3 Sequence 3, Appli  
38 304.5 18.9 93 3 US-09-724-864-61 Sequence 61, Appl  
39 304.5 18.9 358 4 US-09-170-496D-186 Sequence 186, App  
40 304 18.8 342 4 US-09-054-272-2 Sequence 2, Appli  
41 304 18.8 342 4 US-09-826-509-555 Sequence 555, App  
42 303 18.8 326 1 US-08-118-270-39 Sequence 39, Appl  
43 303 18.8 326 5 PCT-US93-08528-39 Sequence 39, Appl  
44 302.5 18.7 373 2 US-08-559-524A-4 Sequence 4, Appli  
45 302.5 18.7 373 3 US-08-749-707-4 Sequence 4, Appli

#### ALIGNMENTS

RESULT 1  
US-09-422-869-20  
; Sequence 20, Application US/09422869  
; Patent No. 6235481  
; GENERAL INFORMATION:  
; APPLICANT: POLONSKY, KENNETH S.  
; APPLICANT: HORIKAWA, YUKIO  
; APPLICANT: ODA, NAOHISA  
; APPLICANT: COX, NANCY J.  
; APPLICANT: SREENAN, SEAMUS  
; APPLICANT: ZHOU, YUN-PING  
; APPLICANT: OTANI, KENICHI  
; APPLICANT: HANIS, CRAIG L.  
; APPLICANT: BELL, GRAEME I.  
; TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES  
; FILE REFERENCE: ARCD:307  
; CURRENT APPLICATION NUMBER: US/09/422,869  
; CURRENT FILING DATE: 1999-10-21  
; EARLIER APPLICATION NUMBER: 60/134,175  
; EARLIER FILING DATE: 1999-05-13  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Human  
US-09-422-869-20

Query Match 100.0%; Score 1614; DB 3; Length 309;  
Best Local Similarity 100.0%; Pred. No. 7.1e-130;  
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNGYNTCGSSDLTPWPAIKLGFYALGVLLVGLLLSLALWVFCRCRQQTETRIYMT 60  
Db 1 MNGYNTCGSSDLTPWPAIKLGFYALGVLLVGLLLSLALWVFCRCRQQTETRIYMT 60  
QY 61 NLAVADICLICLTPFVLSLRDTSPLCOLSQGLYLTNRYSISLVTATAVDVYVVRH 120  
Db 61 NLAVADICLICLTPFVLSLRDTSPLCOLSQGLYLTNRYSISLVTATAVDVYVVRH 120  
QY 121 PLRAGRLSPROAAACAVLWLVIGSLVARLLQEGGFCFRSTRHNSMRFPPLGF 180  
Db 121 PLRAGRLSPROAAACAVLWLVIGSLVARLLQEGGFCFRSTRHNSMRFPPLGF 180  
QY 181 YLPLAVVVFCSLKVVYVTAQAQRPTDVQAEATKAAVMWVWVNLVVFVCFPLHVLTVR 240  
Db 181 YLPLAVVVFCSLKVVYVTAQAQRPTDVQAEATKAAVMWVWVNLVVFVCFPLHVLTVR 240  
QY 241 LAVGNACALLETIRALYITSKLSDANCLDAICYYVMKEFOEASALAVAPRAKAKHS 300

Db 241 LAVGNACALLETIRRALYITSKLSDANCCDAICYVYMAKEFQEASALAVAPRAKAHKS 300  
QY 301 QDSLVCVTLA 309  
Db 301 QDSLVCVTLA 309  
RESULT 2  
US-08-781-250-2  
; Sequence 2, Application US/08781250  
; Patent No. 6010877  
; GENERAL INFORMATION:  
; APPLICANT: Sathe, Ganesh  
; APPLICANT: Van Horn, Stephanie  
; APPLICANT: Bergsma, Derk  
; APPLICANT: Mao, Joyce Yue  
; TITLE OF INVENTION: CDNA CLONE HBSC41 THAT ENCODES A NOVEL 7-TRANSMEMBRAN  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/781,250  
; FILING DATE: 10-JAN-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: William T. Han,  
; REGISTRATION NUMBER: 34,344  
; REFERENCE/DOCKET NUMBER: ATG50043  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610-270-5219  
; TELEFAX: 610-270-4060  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 370 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-781-250-2  
Query Match 24.9%; Score 402; DB 3; Length 370;  
Best Local Similarity 34.1%; Pred. No. 1.3e-26;  
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;  
QY 25 AVLGVLVGLLNSLALWVFCRMOQWTTETRIYMTNLAVADICLLCTLPF-VLHSLR-- 81  
Db 44 AVYSVVFIILGILNVSLSVFCFRMKWRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103  
QY 82 -DSDTPPLCQSGIYLTNRYMSISLVTAIVDRYVAVRHPLRARGLRSPROAAVCAVL 140  
Db 104 WPEGDT-LCKISGTAFTNIYGSMLFTCTSDRFLAIVYPPRSRTIRTRNSAIVCAGV 162  
QY 141 WLVLGSLVARWLLGQEG-----GGFCFRSTRHNFSMR--FPLLGFYLPVAVVVF 189  
Db 163 WLVLSSGGISASLFSSTNNNATTCFEGFSKRWKLYLSKITIFTEVVGFIPLINVS 222  
QY 190 CSLKVVYTAQAQRPPTDVQQAET--RKAARMVMWANLLVFVVCFLPLHVLGTLVRLAVGNAC 248  
Db 223 CSSVVLRLT--RKPATLSQIGTNKKVKLWITVHMAVFFVVCVFPYNSVLFVLVALVRSQAI 280

QY 249 --ALLETIRRALY-ITSKLSANCCDAICYVYMAKEFQEASALAVAPRAKAHKSQDSLC 305  
Db 281 TNCFLERFAKIMPIITLCLATLNCDFPIYFTUESFKSPYI-----NAHIRMESLF 334  
QY 306 VT 307  
Db 335 KT 336  
RESULT 3  
US-09-170-496D-108  
; Sequence 108, Application US/09170496D  
; Patent No. 6555339  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Liaw, Chen W.  
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: AREN-0040  
; CURRENT APPLICATION NUMBER: US/09/170,496D  
; CURRENT FILING DATE: 1998-10-13  
; NUMBER OF SEQ ID NOS: 294  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 108  
; LENGTH: 387  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-170-496D-108  
Query Match 22.8%; Score 368.5; DB 4; Length 387;  
Best Local Similarity 34.3%; Pred. No. 9.6e-24;  
Matches 95; Conservative 48; Mismatches 105; Indels 29; Gaps 11;  
QY 27 LGVLLVGLLNSLALWVFCRMOQWTTETRIYMTNLAVADICLLCTLPFVL-----HSLR 81  
Db 34 LGLEFIFGLLGNGLALWIFCFHLKSKSRIFLFLNLAADVADFLLIICLPVMDYVYVRRSDW 93  
QY 82 DSDTPPLCQSGIYLTNRYMSISLVTAIVDRYVAVRHPLRARGLRSPROAAVCAVLW 141  
Db 94 NFGDIP-CRLVLFMFPMNRQSGIIFLTVAVDYRFRVPHHFNKISNWTAAIISCLLW 152  
QY 142 VLIVIG--SLVARWLLGQEG--GFCFR-STRHNE--NSMRFPILGFYLPVAVVFCSLK 193  
Db 153 GITVGLTVHLLKKKLL-IQNGPANVCISFSICHTFRWHEAMF-LLEFLPLGLIILFCSAR 210  
QY 194 VVYTAQAQRPPTDVQQAETRKAARMVMWANLLVFVVCFLPLHVLGTLVRLAVGW-----N 246  
Db 211 IIVSLRQR--QMDRHAKIKRAITIMVVAIVVICFLP--SVVVRIRIFWLLHTSGTQ 264  
QY 247 ACALLETIRRALYITSKLSDANCCDAICYVYMAKEF 283  
Db 265 NCEVRSVDLAPFITLSFTYNSMLDPVVVYFSPSF 301

RESULT 4  
US-09-170-496D-222  
; Sequence 222, Application US/09170496D  
; Patent No. 6555339  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Liaw, Chen W.  
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: AREN-0040  
; CURRENT APPLICATION NUMBER: US/09/170,496D  
; CURRENT FILING DATE: 1998-10-13  
; NUMBER OF SEQ ID NOS: 294  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 222  
; LENGTH: 387



Db 234 HLIIFCFVPYNINILYSLVRTQTFVNCVVAARVTWYPITLCLIAVSNCCFDPVYVF 293  
QY 279 MAKEFOEA 286  
Db 294 TSDTIQNS 301

RESULT 7  
US-08-467-947A-8  
; Sequence 8, Application US/08467947A  
; Patent No. 6090575  
; GENERAL INFORMATION:  
; APPLICANT: LI, YI  
; APPLICANT: CAO, LIANG  
; APPLICANT: NI, JIAN  
; APPLICANT: GENTZ, REINER  
; APPLICANT: BULT, CAROL J.  
; APPLICANT: SUTTON III, GRANGER G.  
; APPLICANT: ROSEN, CRAIG A.  
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVE., NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467,947A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04079  
; FILING DATE: 30-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 344 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-467-947A-8

Query Match 22.4%; Score 361.5; DB 3; Length 344;  
Best Local Similarity 29.2%; Pred. No. 3.4e-23;  
Matches 90; Conservative 68; Mismatches 107; Indels 43; Gaps 10;  
QY 10 SSDLTWPPAIKLGFYAYL-GVLLVLGLLINSIALWVFCRCMQOWTETRIYMTNLAVADLC 68  
Db 6 SHSCFYNDSPKTYLCMFMSWVFLGLISNCVAIYIFICVLKVRNFTTYMINLAMSDDL 65  
QY 69 LLCTLPFVLHSLRDTSDTP----LCOLSQGIYLTNRYSISLVTATADVRYAVRHLPLRA 124  
Db 66 FVFTLPFRIFYF-TTRNWPFGDLLCKISWMLFTNNYGSILFETCISVDRFLAIVYVFKS 124  
QY 125 RGLSRPQAAVCAVLWLVLI-GSLVARMILGTOEGG-----FCFRSTRHNFNSMFPF-- 176  
Db 125 KTLKTRKNAKIVCTGVMLTVIGGSAPAVFVQSTHSQGNNAACFEN-----FPEA 175

QY 177 -----LLGFYLPNAVVFGLSKVVTALAQRPPTDVGQAEATR-KAARMVMA 221  
Db 176 TKMTYLSRIVFIEIVGFIFILINVTCTSSMWLKLTK--PVTLSRSKINKTKVKMIFV 233  
QY 222 NLLVFWCFLPHVGLTVRLAVGNA---CALLETIRRALYITSKLSANDCCDAICYY 278  
Db 234 HLIIFCFVPYNINILYSLVRTQTFVNCVVAARVTWYPITLCLIAVSNCCFDPVYVF 293  
QY 279 MAKEFOEA 286  
Db 294 TSDTIQNS 301

RESULT 8  
US-08-467-948A-30  
; Sequence 30, Application US/08467948A  
; Patent No. 5998164  
; GENERAL INFORMATION:  
; APPLICANT: LI, YI  
; APPLICANT: CAO, LIANG  
; APPLICANT: NI, JIAN  
; APPLICANT: GENTZ, REINER  
; APPLICANT: BULT, CAROL J.  
; APPLICANT: SUTTON III, GRANGER G.  
; APPLICANT: ROSEN, CRAIG A.  
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVE., NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467,948A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04079  
; FILING DATE: 30-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 302 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide  
US-08-467-948A-30

Query Match 22.3%; Score 360.5; DB 2; Length 302;  
Best Local Similarity 30.0%; Pred. No. 3.6e-23;  
Matches 90; Conservative 64; Mismatches 103; Indels 43; Gaps 10;  
QY 10 SSDLTWPPAIKLGFY-AYLGVLLVLGLLINSIALWVFCRCMQOWTETRIYMTNLAVADLC 68  
Db 1 SENCSTEDSFKTYLKGCVFSWVFLGLIANCVAIYIFTTLKVRNFTTYMLAISDDL 60  
QY 69 LLCTLPFVLHSLRDTSDTP----LCOLSQGIYLTNRYSISLVTATADVRYAVRHLPLRA 124

Db 61 FVETLPPFRYYF-VVRNPFQJVLCKISVTLFVTNNMYGSLFLTCISVDRFLAIVHPFRS 119  
QY 125 RGLSPROAAVCAVLWLV1-GSLVARWLLG1QEGGFCFRST-RHNFNSMR-----FP- 176  
Db 120 KTLRTKRNARIVCAVWITVLGSPASF-----FQSTNRQNTTEQRTCFENFPE 169  
QY 177 -----LLGFYPLAVVVFCSLKVVTALAQRPPTDVQQAETRAKAAWVA 221  
Db 170 STWKTVLSRVIVFIEIVGFIFLILNVCTSTWVLR1L-NKPLTSLRNKLSKKKVLKMFV 228  
QY 222 NLLVFWVFCPLPHVGL---TVRLAVGNACALLETIRRALYITSKLSDANCCLDACYYY 278  
Db 229 HLVIFFCFVPYNTILILYSLMRTQWNCVSVTVAVRTPVTLCAVSNCCFDPVIVYF 288

RESULT 9

US-08-467-947A-30  
; Sequence 30, Application US/08467947A  
; Patent No. 6090575  
; GENERAL INFORMATION:  
; APPLICANT: LI, YI  
; APPLICANT: CAO, LIANG  
; APPLICANT: NI, JIAN  
; APPLICANT: GENTZ, REINER  
; APPLICANT: BULT, CAROL J.  
; APPLICANT: SUTTON III, GRANGER G.  
; APPLICANT: ROSEN, CRAIG A.  
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein  
; TITLE OF INVENTION: Coupled Receptor GPR1  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVE., NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467,947A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04079  
; FILING DATE: 30-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 302 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide  
US-08-467-947A-30

Query Match 22.3%; Score 360.5; DB 3; Length 302;  
Best Local Similarity 30.0%; Pred. No. 3.6e-23;  
Matches 90; Conservative 64; Mismatches 103; Indels 43; Gaps 10;  
QY 10 SSDLTWPPAKLGFY-AYLGVLLVGLLNSLALWVFCRCMQQWTEIRIYMTNLAVADLC 68  
Db 1 SSNCSTEDSFKTYLGCVFMSVFLGLIANCAVIAIFTLKVRNETTTTMYLMLAISDLL 60

QY 69 LLCTLPFVLHSLURDSDTP-----LCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRA 124  
Db 61 FVETLPPFRYYF-VVRNPFQJVLCKISVTLFVTNNMYGSLFLTCISVDRFLAIVHPFRS 119  
QY 125 RGLSPROAAVCAVLWLV1-GSLVARWLLG1QEGGFCFRST-RHNFNSMR-----FP- 176  
Db 120 KTLRTKRNARIVCAVWITVLGSPASF-----FQSTNRQNTTEQRTCFENFPE 169  
QY 177 -----LLGFYPLAVVVFCSLKVVTALAQRPPTDVQQAETRAKAAWVA 221  
Db 170 STWKTVLSRVIVFIEIVGFIFLILNVCTSTWVLR1L-NKPLTSLRNKLSKKKVLKMFV 228  
QY 222 NLLVFWVFCPLPHVGL---TVRLAVGNACALLETIRRALYITSKLSDANCCLDACYYY 278  
Db 229 HLVIFFCFVPYNTILILYSLMRTQWNCVSVTVAVRTPVTLCAVSNCCFDPVIVYF 288

RESULT 10

US-09-745-842-17  
; Sequence 17, Application US/09745842  
; Patent No. 6762029  
; GENERAL INFORMATION:  
; APPLICANT: Conley, Pamela B.  
; APPLICANT: Jantzen, Hans-Michael  
; APPLICANT: Ramakrishnan-DuBridge, Vanitha  
; APPLICANT: Julius, David  
; APPLICANT: Holloper, Gunter  
; APPLICANT: COR Therapeutics, Inc.  
; TITLE OF INVENTION: P2Y12 Receptor  
; FILE REFERENCE: 44481-5053-US  
; CURRENT APPLICATION NUMBER: US/09/745,842  
; CURRENT FILING DATE: 2000-12-26  
; PRIOR APPLICATION NUMBER: US 60/171,622  
; PRIOR FILING DATE: 1999-12-23  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 377  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: P2Y2 purinergic receptor; p2ur  
US-09-745-842-17

Query Match 20.5%; Score 330.5; DB 4; Length 377;  
Best Local Similarity 33.1%; Pred. No. 1.6e-20;  
Matches 90; Conservative 47; Mismatches 108; Indels 27; Gaps 8;

QY 28 GVLLVGLLNSLALWVFCRCMQQWTEIRIYMTNLAVADLCCLTLPFVLHSLURDSDTP 87  
Db 41 GVVCVGLCLNAVALYIFLCRLKTNASTTYMFHLAVSDALYAAASLPLLVYTYARGDHP 100  
QY 88 ----LCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLSPROAAVCAVLWVL 143  
Db 101 FSTVLCKLVRFLFTNLVCSILFLTCISVHRCLGLRPLRSRWRGARYARVAGAVVWL 160  
QY 144 VIG--SLVARWLLG1QEGGFCFRSTRN-----FNSMRFPFLGLFYLPLAVVVF 189  
Db 161 VLACQAPVLYFVTTARGG---RVCHDTSAPELSRFRVAYSSVLMGLL-FAVPPAVILV 216  
QY 190 CSLKVVTALAQRPPTDVQQAETRAKAAWVWVWVLLVFWVCFPLHVLGTLVRLAVGW-- 245  
Db 217 CVVLMARLL-KPAYGTSGGLPRAKRSVRTIAVLAVALFALCFPLPHVTRTLVYSPRSLD 275  
QY 246 NACALLETIRRALYITSKLSDANCCLDACYYY 277  
Db 276 LSCHTLNAINMAYKVTRFLASANSCLDPVLYF 307

RESULT 11

US-09-102-710B-3  
; Sequence 3, Application US/09102710B  
; Patent No. 6479630



209	Qy	AAATKAKARAWWANLVFVWCELPLHUGLTVRLAVGN-----ACALLETIRALYITSK	263
210		:          :          :          :          :          :          :	
211	Db	SPLRKSTVLVILVITVFAVSLPFPVNMKTLNLRALDFQTPQCAFNDKVYATYQVTRG	300
212		:          :          :          :          :          :          :	
264	Qy	LSDNACCLDAICYYTMAKEFOEASALAVAPRAKHSQDSL	304
265		:          :          :          :          :          :          :	
301	Db	LASLNSCDVPIVLYLAGDTFR--PLSRATKSSRRRSEPNV	339
302		:          :          :          :          :          :          :	

## RESULT 13

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US-09-585-876-2
; Sequence 2, Application US/09585876
; Patent No. 6586205
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: 43239, A No. 6586205el GPCR-Like Molecule and
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: 5800-88
; CURRENT APPLICATION NUMBER: US/09/585,876
; CURRENT FILING DATE: 2000-06-01
; EARLIER APPLICATION NUMBER: 60/192,061
; EARLIER FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-585-876-2

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Query Match 19.8%; Score 319.5; DB 4; Length 346;  
Best Local Similarity 28.8%; Pred. No. 1.3e-19;  
Matches 90; Conservative 63; Mismatches 139;  
Indels 21; Gaps 10;

[illegible]

## RESULT 14

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US-09-745-842-15
; Sequence 15, Application US/09745842
; Patent No. 676209
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; APPLICANT: Jantzen, Hans-Michael
; APPLICANT: Ramakrishnan-DuBridge, Vanitha
; APPLICANT: Julius, David
; APPLICANT: Hollopeter, Gunter
; APPLICANT: COR Therapeutics, Inc.
; TITLE OF INVENTION: P2Y12 Receptor

```

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; FILE REFERENCE: 44481-5053-US
; CURRENT APPLICATION NUMBER: US/09/745,842
; CURRENT FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: US 60/171,622
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Meleagris gallopavo
; FEATURE:
; OTHER INFORMATION: Turkey p2Y nucleotide receptor; tp2ynovel
US-09-745,842-15

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[illegible]

## RESULT 15

US-08-513-974B-373  
 ; Sequence 373, Application US/08513974B  
 ; Patent NO. 6114139  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hinuma, Shuji  
 ; APPLICANT: Hosoya, Masaki  
 ; APPLICANT: Fujii, Ryo  
 ; APPLICANT: Ohtaki, Tetsuya  
 ; APPLICANT: Fukusumi, Shoji  
 ; APPLICANT: Ohgi, Kazuhiro  
 ; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
 ; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
 ; NUMBER OF SEQUENCES: 380  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
 ; STREET: 130 Water Street  
 ; CITY: Boston  
 ; STATE: MA  
 ; ZIP: 02109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/513,974B  
 ; FILING DATE: 14-SEP-1995  
 ; CLASSIFICATION: 536  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/JP95/01599  
 ; FILING DATE: 10-AUG-1995

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, , PRIOR APPLICATION DATA: JP 7-093989
, , APPLICATION NUMBER: JP 7-093989
, , FILING DATE: 19-AUG-1995
, ,
, , PRIOR APPLICATION DATA:
, , APPLICATION NUMBER: JP 7-057186
, , FILING DATE: 16-MAR-1995
, ,
, , PRIOR APPLICATION DATA: JP 7-007177
, , APPLICATION NUMBER: JP 7-007177
, , FILING DATE: 20-JAN-1995
, ,
, , PRIOR APPLICATION DATA:
, , APPLICATION NUMBER: JP 6-326611
, , FILING DATE: 28-DEC-1994
, ,
, , PRIOR APPLICATION DATA: JP 6-270017
, , APPLICATION NUMBER: JP 6-270017
, , FILING DATE: 02-NOV-1994
, ,
, , PRIOR APPLICATION DATA:
, , APPLICATION NUMBER: JP 6-236357
, , FILING DATE: 30-SEP-1994
, ,
, , PRIOR APPLICATION DATA:
, , APPLICATION NUMBER: JP 6-236356
, , FILING DATE: 30-SEP-1994
, ,
, , PRIOR APPLICATION DATA:
, , APPLICATION NUMBER: JP 6-189274
, , FILING DATE: 11-AUG-1994
, ,
, , PRIOR APPLICATION DATA:
, , APPLICATION NUMBER: JP 6-189273
, , FILING DATE: 11-AUG-1945
, ,
, , PRIOR APPLICATION DATA:
, , APPLICATION NUMBER: JP 6-189272
, , FILING DATE: 11-AUG-1994
, ,
, , ATTORNEY/AGENT INFORMATION:
, , NAME: Resnick, David S.
, , REGISTRATION NUMBER: 34,235
, , REFERENCE/DOCKET NUMBER: 45753
, ,
, , TELECOMMUNICATION INFORMATION:
, , TELEPHONE: 617-523-3400
, , TELEFAX: 617-523-6440
, ,
, , INFORMATION FOR SEQ ID NO: 373:
, , SEQUENCE CHARACTERISTICS:
, , LENGTH: 373 amino acids
, , TYPE: amino acid
, , STRANDEDNESS:
, , TOPOLOGY: linear
, ,
, , MOLECULE TYPE: peptide
, ,
US-08-513-9748-373

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Query Match	19.6%;	Score 317;	DB 3;	Length 373;
Best Local Similarity	30.1%;	Pred. No. 2.2e-130;		
Matches 101;	Conservative 54;	Mismatches 130;	Indels 50;	Gaps 11;
Qy	2	NGTYNTCGSSDLTWPPAKILGF-----YAYL-----GVLLVLGLLINSALWVFCR	48	
Db	9	NSTINGTWEGD-----ELGKCRFNEDFKVLLPVSYGVVGLGLCLNVVALLIFLCR	61	
Qy	49	MQOWTETRIYNLNAVADLCLLTPLFPVLRLSDTSDTP-----LCOLSQGIYLTNRYMSI	104	
Db	62	LKIWNASTTYMFHLAVSDLSVAASIPLLVYYYARGDHWPFSTVLCKLVRFLFYTNLYCSI	121	
Qy	105	SLVTAIAVDRAVVRHPLRLARGLSRPQAAACVAVLVLVTGSLVARWLLGIQGGGCFR	164	
Db	122	LFLTCSVHRCGLVRLPLHLSLRWGRARYARVAAVWVVLVL-ACQAPVLYFVTTVSVRGR	180	
Qy	165	STRHN-----FNSMRFPLLGLPYLVLAVVFCSLKAVVTALAOERP--TDVQAE	210	
Db	181	ITCHDTSARELFSHFVAYSSVMGLGL-FAPVPFVILVCVYLMMARRLL-KPAYGTGGDLPR	238	
Qy	211	ATRKAARWVANLVLVFWVCFPLPHVGLTVRLAVGW--NACALLETRIRRALYITSKLSGAN	268	
Db	239	AKRSVETIALVAVFALCFPLFPFHVTRTYLVSFRSLDLSCHTLNAINWAYKITRPLASAN	298	
Qy	269	CCLDAICYYY-----MAKEFOBASALAVAPRAK	296	
Db	299	SCLDPVLYFLAGORLVRFPARDAKPPTEPTSPQAR	333	



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OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 11:31:16 ; Search time 204 Seconds  
(without alignments)  
7459.497 Million cell updates/sec

Title: US-10-083-168-84  
Perfect score: 930  
Sequence: 1 atgaatggcactcaaacac.....tgctgagcctgcgctaa 930

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*  
1: /cgn2\_6/ptodata/1/ina/5A-COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B-COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A-COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B-COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PTUS-COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	920.4	99.0	1875	US-09-422-869-21	Sequence 21, Appli
2	920.4	99.0	49136	US-09-422-869-1	Sequence 1, Appli
3	141.8	15.2	1854	US-09-724-864-29	Sequence 29, Appli
4	111.6	12.0	1098	US-09-170-496D-225	Sequence 225, App
5	111.2	12.0	1089	US-09-170-496D-3	Sequence 3, Appli
6	111.2	12.0	1365	US-09-016-434-1429	Sequence 1429, Ap
7	110	11.8	1098	US-09-170-496D-117	Sequence 117, App
8	110	11.8	1597	US-08-724-974A-1	Sequence 1, Appli
9	110	11.8	1697	US-09-364-425B-26	Sequence 26, Appli
10	109.6	11.8	1089	US-09-170-496D-165	Sequence 165, App
11	92.6	10.0	1128	US-09-170-496D-193	Sequence 193, App
12	91	9.8	1128	US-09-170-496D-201	Sequence 201, App
13	91	9.8	1815	US-09-041-545-1	Sequence 1, Appli
14	91	9.8	1815	US-09-327-925-1	Sequence 1, Appli
15	89	9.6	1167	US-09-826-509-574	Sequence 574, App
16	89	9.6	1317	US-09-016-434-1446	Sequence 1446, Ap
17	87.8	9.4	1128	US-09-711-889-1	Sequence 1, Appli
18	87.8	9.4	1128	US-09-170-068-1	Sequence 1, Appli
19	87.8	9.4	1128	US-09-170-496D-55	Sequence 55, Appli
20	87.8	9.4	1128	US-09-170-496D-69	Sequence 69, Appli
21	87.8	9.4	2582	US-08-480-994-6	Sequence 6, Appli
22	87.8	9.4	2582	US-08-616-844-6	Sequence 6, Appli
23	87.8	9.4	2582	US-08-599-654-6	Sequence 6, Appli
24	87.8	9.4	2582	US-08-485-573-6	Sequence 6, Appli
25	87.8	9.4	2582	US-08-944-868A-6	Sequence 6, Appli
26	87.8	9.4	2582	US-08-944-423A-6	Sequence 6, Appli
27	87.8	9.4	2582	US-08-925-743-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-422-869-21  
; Sequence 21, Application US/09422869  
; Patent No. 6235481  
; GENERAL INFORMATION:  
; APPLICANT: POLONSKY, KENNETH S.  
; APPLICANT: HORIKAWA, YUKIO  
; APPLICANT: ODA, NAOHISA  
; APPLICANT: COX, NANCY J.  
; APPLICANT: SEANAN, SEAMUS  
; APPLICANT: ZHOU, YUN-PING  
; APPLICANT: OTANI, KENICHI  
; APPLICANT: HANIS, CRAIG L.  
; APPLICANT: BELL, GRAEME I.  
; TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES  
; FILE REFERENCE: ARCD:307  
; CURRENT APPLICATION NUMBER: US/09/422,869  
; CURRENT FILING DATE: 1999-10-21  
; EARLIER APPLICATION NUMBER: 60/134,175  
; EARLIER FILING DATE: 1999-05-13  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 1875  
; TYPE: DNA  
; ORGANISM: Human  
US-09-422-869-21

Query Match	99.0%	Score 920.4;	DB 3;	Length 1875;
Best Local Similarity	99.4%	Pred. No. 6.5e-197;		
Matches 924;	Conservative 0;	Mismatches 6;	Indels 0;	Gaps 0;
QY	1	ATGAATGGCACCCTACACACCTGTGGCTCCAGCGACCTCACCTGGCCCCCAGCGATCAAG	60	
Db	576	ATGAATGGCACCCTACACACCTGTGGCTCCAGCGACCTCACCTGGCCCCCAGCGATCAAG	635	
QY	61	CTGGGCTTCTAGCCCTACTTGGGCTCTGTGGTCTAGGCTGTCTGCTCAACAGCCTG	120	
Db	636	CTGGGCTTCTAGCCCTACTTGGGCTCTGTGGTCTAGGCTGTCTGCTCAACAGCCTG	695	
QY	121	GGCTCTGGGCTTCTGTCTGGCGATGCGAGTGCGAGCGACCGCATCTACATGACC	180	
Db	696	GGCTCTGGGCTTCTGTCTGGCGATGCGAGTGCGAGCGACCGCATCTACATGACC	755	
QY	181	AACCTGGGGTGGCGGACCTCTGCCCTGTGTGACCTTTGCCCTTGTGTGACCTCCCTG	240	
Db	756	AACCTGGGGTGGCGGACCTCTGCCCTGTGTGACCTTTGCCCTTGTGTGACCTCCCTG	815	
QY	241	CGAGACACTTACAGACCGCGCTGTGCAGCTCTCCAGGGGATCTACTTACACACAGCG	300	

Db 816 CGAGACACCTCAGACACGCGCTGTGCCAGCTCTCCAGGGCATCTACCTGACCAACAGG 875  
Qy 301 TACATGAGCATCAGCTGTGTACCGCCATCGCGTGGAGCCGCTATGTGGCCGTGGGCAC 360  
Db 876 TACATGAGCATCAGCTGTGTACCGCCATCGCGTGGAGCCGCTATGTGGCCGTGGGCAC 935  
Qy 361 CGCTGCGTGCCTCGCGGGCTGCGGTCCCGAGGAGGCTGCGCGCTGTGCGCGTCTCTC 420  
Db 936 CGCTGCGTGCCTCGCGGGCTGCGGTCCCGAGGAGGCTGCGCGCTGTGCGCGTCTCTC 995  
Qy 421 TGGGTGCTGCTCATCGGCTCCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
Db 996 TGGGTGCTGCTCATCGGCTCCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1055  
Qy 481 TTCTGCTTCAGAGACACCGGACAAATTCAACTCCATGCGGTTCCTGCTGCTGCTGCTGCT 540  
Db 1056 TTCTGCTTCAGAGACACCGGACAAATTCAACTCCATGCGGTTCCTGCTGCTGCTGCTGCT 1115  
Qy 541 TACCTGCCCTCGCGTGTGTCTTCTGCTCCCTGAAGGTGGTGAATGCTGCCCTGGCCAG 600  
Db 1116 TACCTGCCCTCGCGTGTGTCTTCTGCTCCCTGAAGGTGGTGAATGCTGCCCTGGCCAG 1175  
Qy 601 AGGCCACCCACGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660  
Db 1176 AGGCCACCCACGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1235  
Qy 661 GCCAACCTCCTGCTGT 720  
Db 1236 GCCAACCTCCTGCTGT 1295  
Qy 721 CTCGAGTGGGTGGAACGCTGTGCCCTCCTGGAGAGCATCCGTGGCCCTGTACATA 780  
Db 1296 CTCGAGTGGGTGGAACGCTGTGCCCTCCTGGAGAGCATCCGTGGCCCTGTACATA 1355  
Qy 781 ACCAGAACCTCTCAGATGCCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840  
Db 1356 ACCAGAACCTCTCAGATGCCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1415  
Qy 841 AAGGAGTTCAGAGGCGTCTGACATGGCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
Db 1416 AAGGAGTTCAGAGGCGTCTGACATGGCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1475  
Qy 901 CAGGACTCTCTGTGTGACCTTCGCTAA 930  
Db 1476 CAGGACTCTCTGTGTGACCTTCGCTAA 1505

## RESULT 2

US-09-422-869-1

; Sequence 1. Application US/09422869

; Patent No. 6235481

; GENERAL INFORMATION:

; APPLICANT: POLONSKY, KENNETH S.

; APPLICANT: HORIKAWA, YUKIO

; APPLICANT: ODA, NAOHISA

; APPLICANT: COX, NANCY J.

; APPLICANT: SREENAN, SEAMUS

; APPLICANT: ZHOU, YUN-PING

; APPLICANT: OTANI, KENICHI

; APPLICANT: HANIS, CRAIG L.

; APPLICANT: BELL, GRAEME I.

; TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES

; FILE REFERENCE: ARCD:307

; CURRENT APPLICATION NUMBER: US/09/422,869

; CURRENT FILING DATE: 1999-10-21

; EARLIER APPLICATION NUMBER: 60/134,175

; EARLIER FILING DATE: 1999-05-13

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 49136

; TYPE: DNA

; ORGANISM: Human

US-09-422-869-1

Query Match 99.0%; Score 920.4; DB 3; Length 49136;

Best Local Similarity 99.4%; Pred. No. 1.3e-196;

Matches 924; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGAATGACACTACAAACACCTGTGGTCCAGCGACCTCACCTGCGCCCGCCAGCGATCAAG 60  
Db 43645 ATGAATGACACTACAAACACCTGTGGTCCAGCGACCTCACCTGCGCCCGCCAGCGATCAAG 43704  
Qy 61 CTGGGCTTTCTACGCTACTTGGGGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120  
Db 43705 CTGGGCTTTCTACGCTACTTGGGGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 43764  
Qy 121 GGGCTCTGGGTGTCTGCTGCGCATGAGAGTGGAGCGGAGACCGGATCTACATGACC 180  
Db 43765 GGGCTCTGGGTGTCTGCTGCGCATGAGAGTGGAGCGGAGACCGGATCTACATGACC 43824  
Qy 181 AACCTGGCGGTGGCGGACCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240  
Db 43825 AACCTGGCGGTGGCGGACCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 43884  
Qy 241 CGAGACACTCAGACACCGCGCTGT 300  
Db 43885 CGAGACACTCAGACACCGCGCTGT 43944  
Qy 301 TACATGAGCATCAGCTGTGTCAAGGCGATCGCGTGGAGCCGCTATGTGGCCGTGGGCGAC 360  
Db 43945 TACATGAGCATCAGCTGTGTCAAGGCGATCGCGTGGAGCCGCTATGTGGCCGTGGGCGAC 44004  
Qy 361 CGGCTGCGTGGCGCGGCTGCGGTCCCGCAGGAGGTGCGGCGGTGTGCGCGGTCTCTC 420  
Db 44005 CGGCTGCGTGGCGCGGCTGCGGTCCCGCAGGAGGTGCGGCGGTGTGCGCGGTCTCTC 44064  
Qy 421 TGGGT 480  
Db 44065 TGGGT 44124  
Qy 481 TTCTGCTTCAGAGACACCGGCGACAAATTCAACTCCATGCGGTTCGCGTGTGGGATTC 540  
Db 44125 TTCTGCTTCAGAGACACCGGCGACAAATTCAACTCCATGCGGTTCGCGTGTGGGATTC 44184  
Qy 541 TACCTGCCCTCGCGCGT 600  
Db 44185 TACCTGCCCTCGCGCGT 44244  
Qy 601 AGGCCACCCACGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660  
Db 44245 AGGCCACCCACGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 44304  
Qy 661 GCCAACCTCCTGCTGT 720  
Db 44305 GCCAACCTCCTGCTGT 44364  
Qy 721 CTCGAGTGGGCTGGAAAGCGCTGTGCCCTCCTGGAGAGCATCCGTGCGCGCCCTGTACATA 780  
Db 44365 CTCGAGTGGGCTGGAAAGCGCTGTGCCCTCCTGGAGAGCATCCGTGCGCGCCCTGTACATA 44424  
Qy 781 ACCAGAACCTCTCAGATGCCAACTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840  
Db 44425 ACCAGAACCTCTCAGATGCCAACTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 44484  
Qy 841 AAGGAGTTCAGAGGCGTCTGACATGGCGGTGGCTCCCGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900  
Db 44485 AAGGAGTTCAGAGGCGTCTGACATGGCGGTGGCTCCCGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 44544  
Qy 901 CAGGACTCTCTGT 930  
Db 44545 CAGGACTCTCTGT 44574

RESULT 3

US-09-724-864-29



US-09-170-496D-3

```
Query Match      12.0%; Score 111.2; DB 4; Length 1089;
Best Local Similarity 50.3%; Pred. No. 1e-15;
Matches 309; Conservative 0; Mismatches 293; Indels 12; Gaps 1;

QY 98 TAGGCTGTCTCAACAGCCCTGGGGCTCTGGGTGTTCTGCTGCGCATGCAAGCAGTGA 157
Db 89 TGGGGCTGCCACCAACTGCTGGCTCTGTGGGGCGCTACCGCCAGGTGCAACAGCGCA 148

QY 158 CGAGACCCGCATCTACATGACCAACCTGGCGGTGGCGACCTCTGCTGCTGTGACCT 217
Db 149 ACGAGTGGGGCTCTACCTGATGAACCTCAGCATCGCCGACCTGTGTACATCTGACGC 208

QY 218 TGCCCTTCTGTGTGCTACCTCCCTGGAGAC-----ACCTCAGACACCGCTGT 265
Db 209 TGCCGCTGTGGTGGACTACTTCTTGACACAGCAAACTGGATCAACGGCCCGGTCT 268

QY 266 GCAGCTCTCCAGGCGATCTACCTGACCAACAGGTACATGAGCATCAGCTGGTCAACGG 325
Db 269 GCAAGCTCTTGGGTTCATCTTACACCAATATCTACATCAGCATGCGCTTCTGTGCT 328

QY 326 CCATCGCGTGAACCGCTATGTGGCGGTGGCGACCCGCTGCGTGCCTGGCGGTGCGGT 385
Db 329 GCATCTCGGTGGACCGCTACCTGGCTGTGGCCACCACTCGGCTTGGCCGCTGGCC 388

QY 386 CCCCAGGACGCTGGCGGTGGCGGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 445
Db 389 GCGTCAAGACCCCGGTGGCGGTGAGCTCGGTGCTGGGCCACGAGCTGGGGCGCACT 448

QY 446 TGCGTCTGCTGCTCTGGGGATTACAGAGGGCGGTCTGCTTTCAGAGACACCCGCGACA 505
Db 449 CGCGGCGCTGTTCATGACGAGCTTCCGAGACCGCTACCAACACACTTCTGCTTTG 508

QY 506 ATTTCAACTCCATGCGGTTCGCGTCTGGATTTCTACCTGCCCTTGGCGGTGGTCT 565
Db 509 AGAAGTTCCCATGGAAGCTGGGTGGCTGGATGAACCTCTATCGGGTTCGTGGGT 568

QY 566 TCTGCTCCCTGAAGTGTGACTGCGCTGGCCAGAGGCCACCCAGAGTGGGGCAGG 625
Db 569 TCCCTCTTCCTGGGGCGCTCATGCTGCTGCTGTAACGGGGCATCTGTCGGGGCGGTG 628

QY 626 CAGAGGCCACCGCAGGCTAAAGCATGCTTGGGCCAACTCTGCTGCTGCTGCTGCTG 685
Db 629 GCAGCGTGTCCACGAGCCCGAGGAGGCCAAGATCAAGCGGTGGCCCTCAGCCTCA 688

QY 686 GCTTCTGCCCTG 699
Db 689 TCGCCATCGTGTG 702
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RESULT 6

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US-09-016-434-1429
; Sequence 1429, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1429:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1365 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9598152
; US-09-016-434-1429

Query Match      12.0%; Score 111.2; DB 4; Length 1365;
Best Local Similarity 50.3%; Pred. No. 1.1e-15;
Matches 309; Conservative 0; Mismatches 293; Indels 12; Gaps 1;

QY 98 TAGGCTGTCTCAACAGCCCTGGGGCTCTGGGTGTTCTGCTGCGCATGCAAGCAGTGA 157
Db 305 TGGGGCTGCCACCAACTGCTGGCTCTGTGGGGCGCTACCGCCAGGTGCAACAGCGCA 364

QY 158 CGAGACCCGCATCTACATGACCAACCTGGCGGTGGCGACCTCTGCTGCTGTGACCT 217
Db 365 ACGAGCTGGGGCTCTACCTGATGAACCTCAGCATCGCGACCTGTGTACATCTGACGC 424

QY 218 TGCCCTTCTGTGTGCTACCTCCCTGGAGAC-----ACCTCAGACACCGCTGT 265
Db 425 TGCCCTTCTGTGTGCTACCTCCCTGGAGAC-----ACCTCAGACACCGCTGT 484

QY 266 GCAGCTCTCCAGGCGATCTACCTGACCAACAGGTACATGAGCATCAGCTGGTCAACGG 325
Db 485 GCAAGCTCTTGGGTTCATCTTACACCAATATCTACATCAGCATGCGCTTCTGTGCT 544

QY 326 CCATCGCGTGAACCGCTATGTGGCGGTGGCGACCCGCTGCGTGCCTGGCGGTGCGGT 385
Db 545 GCATCTCGGTGGACCGCTACCTGGCTGTGGCCACCACTCGGCTTGGCCGCTGCGGC 604

QY 386 CCCCAGGACGCTGGCGGTGGCGGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 445
Db 605 GCGTCAAGACCCCGGTGGCGGTGAGCTCGGTGCTGGGCCACGAGCTGGGGCGCACT 664

QY 446 TGCGTCTGCTGCTCTGGGGATTACAGAGGGCGGTCTGCTTTCAGAGACACCCGCGACA 505
Db 665 CGCGGCGCTCTTCCATGACGAGCTTCTCCGAGACCGCTACCAACACACTTCTGTGTTG 724

QY 506 ATTTCAACTCCATGCGGTTCGCGTCTGGGATTTCTACCTGCCCTTGGCGGTGGTGTCT 565
Db 725 AGAAGTTCCCATGGAAGCTGGGTGGCTGGATGAACCTCTATCGGGTTCGTGGGTCT 784

QY 566 TCTGCTCCCTGAAGTGTGACTGCGCTGGCCAGAGGCCACCCAGAGTGGGGCAGG 625
Db 785 TCTCTTCCCGTGGGCGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 844

QY 626 CAGAGGCCACCGCAGGCTAAAGCATGCTTGGGCCAACTCTGCTGCTGCTGCTGCTG 685
Db 845 GCAGCGTGTCCACGAGCCCGAGGAGGCCAAGATCAAGCGGTGGCCCTCAGCCTCA 904

QY 686 GCTTCTGCCCTG 699
Db 905 TCGCCATCGTGTG 918
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RESULT 7  
US-09-170-496D-117  
; Sequence 117, Application US/09170496D  
; Patent No. 6555339  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Liaw, Chen W.  
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: AREN-0040  
; CURRENT APPLICATION NUMBER: US/09/170,496D  
; CURRENT FILING DATE: 1998-10-13  
; NUMBER OF SEQ ID NOS: 294  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 117  
; LENGTH: 1098  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-170-496D-117

Query Match 11.8%; Score 110; DB 4; Length 1098;  
Best Local Similarity 50.2%; Pred. No. 1.9e-15;  
Matches 402; Conservative 0; Mismatches 365; Indels 33; Gaps 4;  
QY 87 CCTGTGTGTAGGCTGCTCTCAACAGCGCTGGCGTCTGGGTGTCTGTGCGGCAT 146  
DB 90 CGTGTGTGTGGGCTTCCCGGCAACTGCTGTCCCTCTACTTCGGCTACCTGAGAT 149  
QY 147 GCAGAGTGGACGAGACCGCATCTACATGACCACTGGCGGTGGCGGACCTGTGCT 206  
DB 150 CAAGGCCCGGACGAGCTGGGCGTGTACCTGTGCAACCTGACGCTGGCGGACCTTCTA 209  
QY 207 GCTGTGACCTTGGCTTGTCTGCTGCACTCCCTGCGAGACCTCAGACACGCGGTGTG 266  
DB 210 CATCTGTCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 269  
QY 267 CCAGCTCTCCAGGGCATCTACTGACC-----AACAGGTACATGAGCATCAG 314  
DB 270 CGACTGTCTCCAGGTGTGGGATCTCTCTGTACGAGACATCTACATCAGGTGGG 329  
QY 315 CTGTGTACGGCCATCGCGTGGACCGTATGTGCGGTGGCGGACCGCTGGGTGGCGCG 374  
DB 330 CTCTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 389  
QY 375 CGGGCTGCGGTCCCCAGGAGCTGCGGCGGTGTGCGGCTGCTGCTGCTGCTGCTGCT 425  
DB 390 CCAGTTCGGGACCTGAAGGGCGGCGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 449  
QY 426 GCTGTGTATCGGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 485  
DB 450 GCTGACGAGCATCTACTTCTGATGACGAGAGGTATCGAGAGGAGGAGGAGGAGGAG 509  
QY 486 TTTCAGGAGACACCGGCAAAATTTCAACTTCATGCGGTTCGCGTCTGCGGATTTACT 545  
DB 510 CGTGTGCTTTGAGCACTACCCCATCCAGGCATGGCAGCGCGCATCAACTACTACGCTT 569  
QY 546 GCCCTTGGCGGTGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 605  
DB 570 CTTGTGTGGCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 629  
QY 606 ACC-----ACCGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 656  
DB 630 CGCGGTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 689  
QY 657 CTGGGCGCAACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 716  
DB 690 GCTCAGCAGCGGTGCTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 749  
QY 717 GCGCTTGCAGTGGGCTGGAACGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 776

DB 750 GCGAGC---GTCTGGGAGCGCAGCTGCGACTTCCCAAGGCGGTTTTCACGCGCTACCA 806  
QY 777 CATACAGCAGAGCTTCTCAGATGCAACTGTGCTGCGGACGCACTCTGTCTACTACTACAT 836  
DB 807 CTCTCTCCCTCTGCTCACCAGCTTCAACTGGCTGCGGACCGCGTGTCTACTGTCTCGT 866  
QY 837 GCGCAAGAGTTCACAGGAGG 856  
DB 867 CAGCGAGACCAACCCACCGG 886

RESULT 8  
US-08-724-974A-1  
; Sequence 1, Application US/08724974A  
; Patent No. 5912335  
; GENERAL INFORMATION:  
; APPLICANT: Derk J. Bergsma, Catherine E. Ellis  
; TITLE OF INVENTION: A No. 5912335el G-Protein Coupled Receptor  
; TITLE OF INVENTION: HUVCT36  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SmithKline Beecham Corporation  
; STREET: 709 Swedeland Road, P.O. Box 1539  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
; COMPUTER: IBM 486  
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/724,974A  
; FILING DATE: October 3, 1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: William T. Han  
; REGISTRATION NUMBER: 34,344  
; REFERENCE/DOCKET NUMBER: ATG50022  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 610 270 5024  
; TELEFAX: 610 270 5090  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1597  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; ANTI-SENSE: No  
US-08-724-974A-1

Query Match 11.8%; Score 110; DB 2; Length 1597;  
Best Local Similarity 50.2%; Pred. No. 2e-15;  
Matches 402; Conservative 0; Mismatches 365; Indels 33; Gaps 4;  
QY 87 CCTGTGTGTGTAGGCTGCTCTCAACAGCTGCGGCTCTGGGTGTCTGTGCTGCGCAT 146  
DB 431 CGTGTGTGTGTGGGCTTCCCGGCAACTGCTGCTTCTACTTCTGCGCTACTGCGAT 490  
QY 147 GCAGCAGTGGACGAGACCGCATCTACATGACCAACTGGCGGTGGCGGACCTCTGCGCT 206  
DB 491 CAGGCCCGGACGAGCTGGGCGTGTACTGTGCAACTGACGCTGGCGGACCTCTTCTA 550  
QY 207 GCTGTGACCTTGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 266  
DB 551 CATCTGCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 610  
QY 267 CCAGCTTCCAGGGGATCTACCTGACC-----AACAGGTACATGAGCATCAG 314

Db 611 CGACCTGTCTGCCAGGTGTGGGCATCTCTGTACGAGAACATCTACATCAGCGTGG 670  
Qy 315 CQTGTCAGGCGCATCGCGTGCAGCTATGTGCGGTGCGCGACCGCTCGTGGCCG 374  
Db 671 CTTCTCTGTCTGCTCATCTCGTGAGCCGCTACTGTGCTGTGGCCATCCCTTCGGTTCCA 730  
Qy 375 CGGGCTGCGGTGCTCCCGCAGCAGCTGCGGCGGTGTGCGGCTCTCTGGG-----T 425  
Db 731 CCAGTTCGGGACCTCGAAGCGCGCTCGGCGTGCAGCGTGTGTCTGCGCCAGAGCT 790  
Qy 426 GCTGTCTATCGGCTCCCTGGTGGCTGCTGGTCTCTGGGATTCAGAGGCGGCTTCTG 485  
Db 791 GCTGACCAAGCATCTCTCTGATGACAGAGGAGTCTATCGAGGACGAGAACAGCACCG 850  
Qy 486 CTTTCAGGAGCACCGGCACAAATTCACATCCATGCGGTTCCCGCTGCTGGGATTTACT 545  
Db 851 CGTGTGCTTTGAGCACTACCCCATCCAGGCATGGCAGCGCCATCAACTACTACCGCTT 910  
Qy 546 GCCCTGCGCGTGTGGTCTTCTGTCTCCCTGAAGGTGTGTGACTGCCCTGGCCCGAGAGCC 605  
Db 911 CTTGTGGGCTTCTCTTCTCCCATCTGCTCTGCTGTGGGCTCTACAGGGCATCTTGG 970  
Qy 606 ACC-----ACCGAGTGGGAGCAGCAGAGCCACCGCAAGGCTAAACGATGTT 656  
Db 971 CGCGCTGCGCGGAGCCACCGCACCCAGAAAGCGCGCAAGGACCAAGATCCAGCGGTGT 1030  
Qy 657 CTGGGCCAACCTCTGGTGTCTGCTGTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 716  
Db 1031 GCTCAGCACCGTGGTCTCTCTGCGCTGCTCTCTGCTGCTCTCTGCTGCTGCTGCT 1090  
Qy 717 GCGCTCTGCGAGTGGGCTGGAAGCGCTGTGCTCTCTGAGAGAGTCCGCTGCGGCTGTA 776  
Db 1091 GCGGAGC---GTCTGGGAGCCAGCTGCGACTTGGCAGGCGGTTTCAACGCTACCA 1147  
Qy 777 CATAACCAAGCAAGCTCTCAGATGCCAACTGCTGCTGCGTGGACGCCATCTGCTACTACAT 836  
Db 1148 CTTCTCCCTCTGCTCACCAGCTTCAACTGCGTGGCGGACCGCTGCTCTGCTGCTCT 1207  
Qy 837 GCGCAAGGAGTTCAGGAGG 856  
Db 1208 CAGCGAGACCCACCCCGGG 1227

RESULT 9

US-09-364-425B-26  
; Sequence 26, Application US/09364425B  
; Patent No. 6653086  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lin, I-Lin  
; APPLICANT: Lowitz, Kevin P.  
; APPLICANT: Chen, Ruoping  
; TITLE OF INVENTION: Endogenous, Constitutively Activated G Protein-Coupled Orphan Receptor  
; FILE REFERENCE: Aren0047  
; CURRENT APPLICATION NUMBER: US/09/364,425B  
; CURRENT FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: 60/094,879  
; PRIOR FILING DATE: 1998-07-31  
; PRIOR APPLICATION NUMBER: 60/106,300  
; PRIOR FILING DATE: 1998-10-30  
; PRIOR APPLICATION NUMBER: 60/110,906  
; PRIOR FILING DATE: 1998-12-04  
; PRIOR APPLICATION NUMBER: 60/121,851  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 26  
; LENGTH: 1697  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-364-425B-26

Query Match 11.8%; Score 110; DB 4; Length 1697;  
Best Local Similarity 50.2%; Pred. No. 2,1e-15;  
Matches 402; Conservative 0; Mismatches 365; Indels 33; Gaps 4;

Qy 87 CQTGTCAGGCTGTGCTGTCTCAACAGAGCTGCGGTCTGGGTGTCTGCTGCGCAT 146  
Db 413 CQTGTCAGGCTGTGCTGTCTCAACAGAGCTGCGGTCTGGGTGTCTGCTGCGCAT 472  
Qy 147 GCAGCAGTGGAGGAGACCCGCATCTATACACCACTGGCGGTGGCGGTGGCGCTCTGCT 206  
Db 473 CAAGGCCGGAACAGAGCTGGCGGTGTCTGTGCAACCTGACGGTGGCGGACCTCTCTTA 532  
Qy 207 GCTGTGCACTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 266  
Db 533 CATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 592  
Qy 267 CAGCTCTCCAGGCGCATCTACTGACC-----AACAGGTATCAGCATCAG 314  
Db 593 CGACCTGCTGCGAGGTGTGCGCATCTCTCTGTACGAGAACATCTATCATCAGCGTGG 652  
Qy 315 CQTGTCAGGCGCATGCGGTGGAGCGCTATGTGCGGTGCGGACCCGCTGCTGCTGCG 374  
Db 653 CTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 712  
Qy 375 GCGGCTGCGGTCTCCCGCAGGCTGCGGCGGTGTGCGGCTGCTCTGCTGCTGCTGCT 425  
Db 713 CAGTTCGCGACCTGAGAGCGCGCTGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 772  
Qy 426 GCTGTCTATCGGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 485  
Db 773 GCTGACCAAGCATCTACTTCTCTGATGACAGAGGCTCATCGAGGACGAGAACAGCACCG 832  
Qy 486 CTTCAGGAGCACCGCGCAATTTCAACTCCATGCGGTTCCTGCTGCTGCTGCTGCTGCT 545  
Db 833 CQTGTCCTTTGAGCACTACCCCATCCAGGCGATGGCAGCGCGCATCAACTACTACGCTT 892  
Qy 546 GCGGCTGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 605  
Db 893 CQTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 952  
Qy 606 ACC-----ACCGAGCTGGGCGCAGCAGAGGCGCACCCGCAAGAGCCAGATCCAGCGGTGT 1012  
Db 953 GCGGCTGCGCGGAGCCACCGCACCCAGAAAGCGCGCAAGGACGAGATCCAGCGGTGT 1072  
Qy 657 CTGGGCGCAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 716  
Db 1013 GCTCAGCACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1072  
Qy 717 GCGGCTGCGAGTGGGCTGGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 776  
Db 1073 GCGGAGC---GTCTGGGAGGCGAGTGGAGTTCGCAAGGCGGTTTTCAACGCTTACCA 1129  
Qy 777 CATAACCAAGCAGCTCTCAGATGCCAACTGCTGCTGCGTGGACGCCATCTGCTACTACTACAT 836  
Db 1130 CTTCTCCCTCTGCTCACCAGCTTCAACTGCGTGGCGGACCGCTGCTGCTGCTGCT 1189  
Qy 837 GCGCAAGGAGTTCAGGAGG 856  
Db 1190 CAGCGAGACCCACCCCGGG 1209

RESULT 10

US-09-170-496D-165  
; Sequence 165, Application US/09170496D  
; Patent No. 655339  
; GENERAL INFORMATION:  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Liaw, Chen W.  
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein Receptor  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: AREN-0040

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; CURRENT APPLICATION NUMBER: US/09/170,496D
;
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 165
; LENGTH: 1089
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496D-165

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Query Match 11.8%; Score 109.6; DB 4; Length 1089;  
Best Local Similarity 52.5%; Pred. No. 2.3e-15;  
Matches 272; Conservative 0; Mismatches 234; Indels 12; Gaps 1;

98	QY	TAGGCTGTGCTCAACAGCCTGGCGCTCTGGGTGTTCTGTGCGCGCATGACAGCAGTGA	157
89	Db	TGGGGCTGCCCAACCAATGCCCTGGCTCTGTGGGGCGCCCTACCGCCAGGTGCAACAGCGCA	148
158	QY	CGGAGACCCGCATCTACATGACCAACCTGGCGGTGGCGGACCTCTGCCTGCTGTGTCACCT	217
149	Db	ACGAGCTGGGGCGTCTACTGTATGAACCTCAGCATGCGCGACCTGCTGTACATCTGCACGC	208
218	QY	TGCCCTTGTGTGCTGACCTCCCTGGAGAC-----ACCTCAGACAGCGCGCTGT	265
209	Db	TGCCGTGTGGGTGGACTACTTCTGTGACCAAGCAACTGATCCACGGCCCGGGTCTCT	268
266	QY	GCCAGCTCTCCACGGGCATCTACCTGACCAACAGGTACATGAGCATCAGCCTGTGTACGG	325
269	Db	GCAAGCTCTTTGGGTTCATCTTCTACACCAATATCTACATCAGCATCGCCTTCCCTGTGCT	328
326	QY	CCATCGCGGTGAACGGTATATGTGGCGGTGGCGCACCCGCTGCGTGCCCGCGGCTGCGGT	385
329	Db	GCATCTCGGTGGACCGCTACCTGGCTGTGGGCCACCCCACTCGCTTCGCGCGCCTGCGCC	388
386	QY	CCCCAGCAGGCTCGCGCGGTGTGGCGGTCTCTTGGTGTCTGTGCTCATCGCTCCCTGG	445
389	Db	CGGTCAAGACCGCGCTGGCGGTGAGCTCCGTGGTCTGGGCGCACGGAGCTGGGCGCGCACT	448
446	QY	TGGCTCGCTGCTCTCTGGGATTCAGGAGGCGGCTTCTGTTCAGGAGACCCCGGCACA	505
449	Db	CGGCGGCCCTGTTCATGACAGACTTCCGAGACCGCTACAAACACACTTCTGCTTTG	508
506	QY	ATTTCAACTCCATCGGTTCCCGCTGTGGGATTCACCTGCCCCCTGGCGCGGTGGTGTCT	565
509	Db	AGAAGTCCCATGGAAGGCTGGGTGGCTGGATGAACCTCTATCGGGGTGTCTGTGGGT	568
566	QY	TCTGCTCCCTGAAGGTGTGACTGCCCTGGCCCCAGAG	603
569	Db	TCCTCTTTCCGTGGCGCTCATGCTGCTGTGCTATCCGG	606

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RESULT 11
US-09-170-496D-193
; Sequence 193, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 193
; LENGTH: 1128
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496D-193

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Query Match 10.0%; Score 92.6; DB 4; Length 1128;

Best Local Similarity	47.9%;	Pred. No. 1.5e-11;
Matches	371; Conservative	0; Mismatches 389; Indels 15; Gaps 3
Qy	66	CTTCTACGGCTACTTGGCGGCTCTCGTCTGGTGGTCTAGGCTGTCTGTCAACAGCTGGCGCT 125
Db	183	CTCGTGCTCTACACCATCTTCCTCTCCCATCGGCTTTGTGGCAACATCCTGATCCT 242
Qy	126	CTGGGTGTTCTGTCCGCGATGCGAGTGGACGGAGACCGCATCTACATGACCAAGCT 185
Db	243	GGTGGTGAACATCAGCTTCCGCGAAGATGACATCCCGACCTGTACTTTCATCAAGCT 302
Qy	186	GGCGGTGGCGAGCTCTGCTGCTGTGTCACACTTGGCCCTTCGTGCTGCATCCCT----- 239
Db	303	GGCGGTGGCGAGCTCTATCTCTGTGGCGGACTCCCTCATTAGGTGTTCAACCTGCACGA 362
Qy	240	GGGAGACACCTCAGACACCGCGCTGTGCCAGCTCTCCAGGGCATCTACCTGACCAACAG 299
Db	363	GGGTACTACGACATCGCGCTCTGTGCACTTCATGTGCTCTTCCTGCAAGTCAACAT 422
Qy	300	GTACATGAGCATCAGCCTGTGTACGGGCAATGGCGTGGACCGCTATGTGGCGGTGGCGCA 359
Db	423	GTACAGCAGCGTCTTCTCTCTCACTGGATGAGCTTCGACCGCTACATCGCCCTGGCCAG 482
Qy	360	CCGCTGCTGTCGGCGGGCTGGGTCCCGAGCAGGCTCGCGCGCTGTGCGCGGTCT 419
Db	483	GGCCATGCGCTGACGCTGTTTCGCGACCAAGCACACGCCCGGCTGAGCTGTGGCCTCAT 542
Qy	420	CTGGGTCTGCTCATCGGCTCCCTGTGTGGCTCGCTGTGCTCTCTGGGATTCAGGAGGGCGG 479
Db	543	CTGGATGGCATCCGTGTACGACAGCTGTGTGCCCTTCACGCCCGTGCACTGTGACGACAC 602
Qy	480	CTTCTGTCTCAGGAGCACCGCGCACAAATTTCAAATCCATGCGGTTCGCGC-----TGCT 533
Db	603	CGAGAGGCCTGTTCTGTGTTTCGCGATGTCCGGAGTGCAGTGGCTCGAGGTCAAGCT 662
Qy	534	GGGATTTCACTGCGCTCGCGGTGTGTCTTCTGTCTCCCTGAAGGTGTGATCGCCCT 593
Db	663	GGGCTTCATCGTGCCTTTCGCCATCATCGGCTGTGCTACTCCCTCATTTGTCGGGTGCT 722
Qy	594	GGCCCCAGAGCCACCCACGACGTGGGGCAGGACAGGCCACCCGACAGGCTTAACGAT 653
Db	723	GGTC---AGGGCGCACCGGACCGTGGGCTGCGGCCCGCGGAGAGGGGAAACGAT 779
Qy	654	GGTCTGGGCCAACTCTCTGTGTTGTGTGTCTGTCTCTGCGCCCTGCACGTGGGCTGCAC 713
Db	780	GATCCTCGCGGTGTGTGTCTTCTTCGTTCTGTCTGTGCTGCCGAGAACGTTCTCATCAG 839
Qy	714	AGTGGCGCTCGCAGTGGGCTGGAAACGCTGTGCCCTCTTGAGACGATTCGTCGGCGCCT 773
Db	840	CGTGCACCTCTGCAGCGGACGACGCTGGGCGGCTCCCTGCAAGCAGTCTTTTCGGCA 899
Qy	774	GTACATAACAGCAAGCTCTCAGATGCCAATGTGTGCTGAGCGCCATCTGCTAC 828
Db	900	TGCCACCCCTCTCACGGGCGCACATTTGTCAACCTCGGCGCTTCTTCCAAACAGCTGC 954

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RESULT 12
US/09-170-496D-201
; Sequence 201, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 201
; LENGTH: 1128
;

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Db 1241 GCCTCTGCTGGTTCATCAGCGTGTTCACCGCGCCATCAT-GTGTGCACTGTGCGGCGCG 1299  
QY 585 GACTGCCCTGGCCAGAGCCACCCAGACCGAGCTGGGGCAGGAGCCACCCGCAAGGC 644  
Db 1300 GTCTGCTCGCCAGGCTCGCCAGCGCGGTCGCGGCCATGACAGTCTCTGCTCACGGTGC 1359  
QY 645 TAAAC 649  
Db 1360 TCATC 1364

RESULT 14  
US-09-327-925-1  
; Sequence 1, Application US/09327925A  
; Patent No. 6096868  
; GENERAL INFORMATION:  
; APPLICANT: SATHE, GANESH M.  
; APPLICANT: HALSEY, WENDY S.  
; APPLICANT: MAO, JOYCE YUE  
; TITLE OF INVENTION: ECR673: A 7 TRANSMEMBRANE G-PROTEIN  
; FILE REFERENCE: GP-70414-1  
; CURRENT APPLICATION NUMBER: US/09/327,925A  
; EARLIER APPLICATION NUMBER: 09/041,545  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 1815  
; TYPE: DNA  
; ORGANISM: HOMO SAPIENS  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: (16)  
US-09-327-925-1

Query Match 9.8%; Score 91; DB 3; Length 1815;  
Best Local Similarity 50.4%; Pred. No. 3.8e-11;  
Matches 305; Conservative 0; Mismatches 290; Indels 10; Gaps 3;  
QY 48 CCCAGCGATCAAGCTGGGCTTCTAGCCCTACTTGGGGCTCTGCTGGTGTAGGCTGCT 107  
Db 767 CCCAGCGCTGGTGGCGCTGATGCGCGTGCACGAGCCATCTCTTGGCAGGGCTGT 826  
QY 108 GCTCAACAGCTGGCGCTCTGGGTGTCTGCTGCCGATGACAGTGGACGAGACCG 167  
Db 827 GCTCAACGGCTGGCGCTGTACGTCTTCTGCTGCCGACCCCGGCCAAGACACCTCAGT 886  
QY 168 CATCTACATGACCAACCTGGCGGTGGCGACCTCTGCTGTGTGCACCTTGGCCCTTGT 227  
Db 887 CATCTACACCATCAACCTGGTGTGACCGATCTACTGTGTAGGGCTGTCCCTGCCACCG 946  
QY 228 GCTGACATCCCTGGCAGACCTCAGACACGCGCTGTGCCAGTCTTCCAGGGATC-- 285  
Db 947 CTTCGCTGTACTACGGCGCCAGGGGCTGCTGGCGCTGTGCTTCCCGCACGTCTCGG 1006  
QY 286 -TACCTGACCAACAGTACATGACATCAGCTGTGTCAAGGCGCATCGCGTGCAGCTA 344  
Db 1007 TTACTTCTCAACATGCACTGTCTTCTCTCTCTCACTGCACTGTGGTGGACCGCTA 1066  
QY 345 TGTGGCGGTGCGGCACCCGCTCGTGTGCCGCGGGCTGGCGGTCCCGCAGGAGCTGCGGC 404  
Db 1067 CTGGCCATCTGTGGCGCTGAGGCTCCGCGCTGCCCGCAGCTGCTGTGCCAGGC 1126  
QY 405 CGTGTGCGGCTCTCTGGGTGCTGGTCAATCGGCTCCCTGTGGTGTGGTGTGCTCTGGG 464  
Db 1127 CGTGTGCGCTCTCTGGTGTGGCTGGCGCGGTGCC-----GTCACTGTCTGGTGTGG 1180  
QY 465 GATTTCAGGAGGGCGCTCTCTGCTTTCAGGAGCACCCGCGACATTTCAACTCCATCGGTT 524  
Db 1181 CGTGACAGGACCGCGCTCTGCTGCGGTGTCTTTGCGGTGACTGTCTTGGTCTCTGCT 1240

QY 525 CCCGCTGCTGGGATTTCTACTGCCCTCCCTGGCGGTGGTGTCTTCTGCTCCCTGAAGGTGT 584  
Db 1241 GCCTCTGCTGGTTCATCAGCGTGTTCACCGCGCCATCAT-GTGTGCACTGTGCGGCGCG 1299  
QY 585 GACTGCCCTGGCCAGAGCCACCCAGACCGAGCTGGGGCAGGAGCCACCCGCAAGGC 644  
Db 1300 GTCTGCTCGCCAGGCTCGCCAGCGCGGTCGCGGCCATGACAGTCTCTGCTCACGGTGC 1359  
QY 645 TAAAC 649  
Db 1360 TCATC 1364

RESULT 15  
US-09-826-509-574  
; Sequence 574, Application US/09826509  
; Patent No. 6806054  
; GENERAL INFORMATION:  
; APPLICANT: Lehmann-Bruinsma, Karin  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lin, I-Lin  
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G  
; FILE REFERENCE: AREN-207  
; CURRENT APPLICATION NUMBER: US/09/826,509  
; CURRENT FILING DATE: 2001-04-05  
; PRIOR APPLICATION NUMBER: 60/195,747  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: 09/170,496  
; PRIOR FILING DATE: 1998-10-13  
; NUMBER OF SEQ ID NOS: 589  
; SOFTWARE: PatentIn Version 2.1  
; SEQ ID NO 574  
; LENGTH: 1167  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-826-509-574

Query Match 9.6%; Score 89; DB 4; Length 1167;  
Best Local Similarity 55.5%; Pred. No. 9.6e-11;  
Matches 217; Conservative 0; Mismatches 165; Indels 9; Gaps 2;  
QY 45 GCCCCAGCGATCAAGCTGGGCTTCTAGCCCTACTTGGGCGTCTGCTGTGCTAGGCTT 104  
Db 126 GCGGCGCGCGGCGATGTCGTATCCAGTGCATCTACGCGCTGTGTGCTTGGTGGGCT 185  
QY 105 GCTGCTCAACAGCTGGCGCTCTGGGTGTCTGCTGCCGCGCATGACGAGTGGACGAGAC 164  
Db 186 GGTGGGCAACGCGCTGGTCACTTTCGTGATCTTTCGTACGCCAAGATGAAGACGGCTAC 245  
QY 165 CCGCATCTACATGACCAACCTGGCGGTGGCGGACCTCTGCCCTGTGTGCACTTGGCTTT 224  
Db 246 CAACATCTACTGCTCAACCTGGCGGTAGCGGCGAGCTCTTCACTGTGAGGTGCTT 305  
QY 225 CGT-----GCTGCACTCCCTGCGAGAC---ACCTCAGACAGCGCGCTGTGCAAGCTTC 275  
Db 306 GGTGGCTCGTGGCGCGCGCTTGGCCACTGGGCGCTTGGCTCGCTGTGCTGCGCGCT 365  
QY 276 CCAGGGCATCTACCTGACCAACAGGTATGAGCATCAGCTGGTGGTGGCCATCGCCCT 335  
Db 366 GCTCAGCGTCAGCGGCTCAACATGTTTCAACAGCGTCTTGTCTCAGCGTCTCAGCT 425  
QY 336 GGACGCTATGTGGCGGTGGCGACCGCTGGGTGCCCGCGGCTGCGGTCCCGCAGGCA 395  
Db 426 GGACGCTATGTGGCGGTGGTGGACCTTCTGGCGCGGGGACCTACCGGCGGCCAGCT 485  
QY 396 GGTGCGCGCGGTGGCGGCTTCTCTGGGTG 426  
Db 486 GGCCAAAGCTCATCAACCTGGGCGGTGTGCTG 516

Search completed: May 23, 2005, 14:02:30  
Job time : 209 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 23, 2005, 11:09:25 ; Search time 58.5 Seconds  
(without alignments)  
2704.829 Million cell updates/sec

Title: US-10-083-168-16  
Perfect score: 1614  
Sequence: 1 MNGTYNTCGSSDLTWPPAIAK.....AVAPRAKAHKSQSLCVTLA 309

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1608	99.6	309	1 GP35_HUMAN	Q9hc97 homo sapien
2	1602	99.3	394	2 Q6ZMP9	Q6zmp9 homo sapien
3	1124	69.6	307	1 GP35_MOUSE	Q9es90 mus musculus
4	1123	69.6	307	2 Q8CB97	Q8cb97 mus musculus
5	1109	68.7	307	2 Q8BS98	Q8bs98 mus musculus
6	402	24.9	370	1 P2Y9_HUMAN	Q99677 homo sapien
7	400	24.8	370	2 Q6NSP5	Q6nsp5 homo sapien
8	400	24.8	370	2 Q8BKK1	Q8bkk1 mus musculus
9	392	24.3	370	2 Q8BLG2	Q8blg2 mus musculus
10	376	23.3	319	2 Q8N580	Q8n580 homo sapien
11	375.5	23.3	363	2 Q8TDS4	Q8tds4 homo sapien
12	368.5	22.8	308	1 P2Y5_CHICK	P32250 gallus gall
13	368.5	22.8	387	1 Q9JB_HUMAN	P49019 homo sapien
14	368.5	22.8	387	2 Q8NGE4	Q8nge4 homo sapien
15	368	22.8	347	2 Q7ZZA4	Q7zza4 brachydanio
16	365.5	22.6	296	2 Q9WU09	Q9wu09 rattus norv
17	362	22.4	372	1 GP92_HUMAN	Q9hlc0 homo sapien
18	361.5	22.4	344	1 P2Y5_HUMAN	P43657 homo sapien
19	361.5	22.4	344	2 Q7Z3S0	Q7z3s0 homo sapien
20	361.5	22.4	344	2 Q7Z3S6	Q7z3s6 homo sapien
21	357.5	22.1	344	1 P2Y5_MOUSE	Q8bmc0 mus musculus
22	348.5	21.6	360	2 Q9EP66	Q9ep66 mus musculus
23	340	21.1	319	2 Q9Y2T6	Q9y2t6 homo sapien
24	338.5	21.0	360	2 Q8OZ39	Q8oz39 rattus norv
25	331.5	20.5	374	1 P2Y2_RAT	P41232 rattus norv
26	331	20.5	298	2 Q8VE54	Q8ve54 mus musculus
27	330.5	20.5	377	1 P2Y2_HUMAN	P41231 homo sapien
28	327	20.3	346	1 GP81_HUMAN	Q9bxc0 homo sapien
29	324	20.1	346	2 Q6NXU5	Q6nxu5 homo sapien
30	322.5	20.0	345	1 CLT2_PIG	Q95n03 sus scrofa
31	321	19.9	349	2 Q6P852	Q6p852 xenopus tro

#### RESULT 1

GP35\_HUMAN

ID GP35\_HUMAN STANDARD; PRT; 309 AA.

AC Q9HC97; O43495; Q86UH4;

DT 16-OCT-2001 (Rel. 40, Created)

DT 29-MAR-2004 (Rel. 43, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Probable G protein-coupled receptor GPR35.

GN Name=GPR35;

OS Homo sapiens (Human);

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98140132; PubMed=9479505; DOI=10.1006/geno.1998.5095;

RA O'Dowd B.F., Nguyen T., Marchese A., Cheng R., Lynch K.R.,

RA Heng H.W.Q., Kolakowski L.F. Jr., George S.R.;

RT "Discovery of three novel G-protein-coupled receptor genes.";

RL Genomics 47:310-313(1998).

RN [2]

RP SEQUENCE FROM N.A., AND VARIANTS THR-25; ILE-29; MET-108; SER-125;

RP MET-253 AND SER-294.

RX MEDLINE=20472315; PubMed=11017071; DOI=10.1038/79876;

RA Horikawa Y., Oda N., Cox N.J., Li X., Orho-Melander M., Hara M.,

RA Hinokio Y., Lindner T.H., Mashima H., Schwarz P.E.H.,

RA del Bosque-Plata L., Horikawa Y., Oda Y., Yoshiuchi I., Colilla S.,

RA Polonsky K.S., Wei S., Concannon P., Iwaaki N., Schulze J.,

RA Baier L.J., Bogardus C., Groop L., Boerwinkle E., Hanis C.L.,

RA Bell G.I.;

RT "Genetic variation in the gene encoding calpain-10 is associated with

type 2 diabetes mellitus.";

RL Nat. Genet. 26:163-175(2000).

RN [3]

RP SEQUENCE FROM N.A., AND VARIANT SER-294.

RA Warren C.N., Aronstam R.S., Sharma S.V.;

RT "cDNA clones of human proteins involved in signal transduction

sequenced by the Guthrie cDNA resource center (www.cdna.org).";

RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Orphan receptor.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

CC -!- TISSUE SPECIFICITY: Expressed in all adult and fetal tissues

examined, including pancreatic islets and skeletal muscle, with

relatively higher levels in adult lung, small intestine, colon and

stomach.

CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

-----  
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[illegible]

DE	Probable G protein-coupled receptor GPR35.
GN	Names=Gpr35;
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RP	MEDLINE=20472315; PubMed=11017071; DOI=10.1038/79876;
RA	Horikawa Y., Oda N., Cox N.J., Li X., Orho-Melander M., Hara M.,
RA	Hinokio Y., Lindner T.H., Mashima H., Schwarz P.E.H.,
RA	dal Bosque-Plata L., Horikawa Y., Oda Y., Yoshiuchi I., Colilla S.,
RA	Polonsky K.S., Wei S., Concanan P., Iwasaki N., Schulze J.,
RA	Baier L.J., Bogardus C., Groop L., Boerwinkle E., Hanis C.B.,
RA	Bell G.I.;
RT	"Genetic variation in the gene encoding calpain-10 is associated with
RT	type 2 diabetes mellitus";
RL	Nat. Genet. 26:163-175(2000).
RP	[2]
RP	SEQUENCE FROM N.A.
RP	STRAIN=C57Bl/6J; TISSUE=Mammary gland;
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Diatchenko I., Marudina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA	Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahay J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Truchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA	Schneerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences.";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC	-1- FUNCTION: Orphan receptor.
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC	-1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation
CC	at the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC	-----
DR	EMBL; AF200349; AA818487.1; -
DR	ENBL; BC027429; AA827429.1; -
DR	MGD; MGI:1929509; Gpr35.
DR	InterPro; IPR000276; GPCR_Rhodopsn.
DR	InterPro; IPR002286; P2_purinoceptor.
DR	Pfam; PF00001; 7tm 1; 1.
DR	PRINTS; PR00237; GPCRHHODOPS.
DR	PROSITE; PS00237; G PROTEIN RECEPTOR FL 1; 1.
DR	PROSITE; PS00262; G PROTEIN RECEPTOR FL 2; 1.
KW	G-protein coupled receptor; Glycoprotein; Transmembrane.
FT	DOMAIN 1 18 Extracellular (Potential).
FT	TRANSMEM 19 39 1 (Potential).
FT	DOMAIN 40 53 Cytoplasmic (Potential).
FT	TRANSMEM 54 74 2 (Potential).
FT	DOMAIN 75 88 Extracellular (Potential).
FT	TRANSMEM 89 110 3 (Potential).
FT	DOMAIN 111 129 Cytoplasmic (Potential).
FT	TRANSMEM 130 150 4 (Potential).
FT	DOMAIN 151 176 Extracellular (Potential).

RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";   
RL Nature 420:563-573 (2002).

[4]  
RN SEQUENCE FROM N.A.  
RP STRAIN=C57BL/6J; TISSUE=Bone;  
RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RX Carninci P. Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RN Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630 (2000).

RNA	[5]	SEQUENCE FROM N.A.
RP		STRAIN=C57BL/60; TISSUE=Bone;
RX		MEDLINE=20330913; PubMed=11076861; DOI=10.1101/gr.152600;
RA		Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA		Konno H., Akiyama J., Nishi K., Kitsumai T., Tashiro H., Itoh M.,
RA		Sumi N., Ishii Y., Nakamura S., Hazama N., Nishine T., Harada A.,
RA		Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA		Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA		Yoneda Y., Ishikawa T., Ozawa Y., Tanaka T., Matsura S., Kawai J.,
RA		Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT		"RIKEN integrated sequence analysis (RISA) system-384-format
RT		sequencing pipeline with 384 multicapillary sequencer.";
RL		Genome Res. 10:1757-1771(2000).

[6]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Bone;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shingagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayaishizaki Y.,  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.





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FT DOMAIN          95 112 Extracellular (Potential).
FT TRANSMEM       113 133 3 (Potential).
FT TRANSMEM       134 155 Cytoplasmic (Potential).
FT TRANSMEM       156 176 4 (Potential).
FT TRANSMEM       177 203 Extracellular (Potential).
FT TRANSMEM       204 224 5 (Potential).
FT TRANSMEM       225 254 Cytoplasmic (Potential).
FT TRANSMEM       255 275 6 (Potential).
FT TRANSMEM       276 294 Extracellular (Potential).
FT TRANSMEM       295 315 7 (Potential).
FT TRANSMEM       316 370 Cytoplasmic (Potential).
FT DISULFID       111 188 By similarity.
FT CARBOHYD       15 15 N-linked (GlcNAc...) (Potential).
FT CARBOHYD       24 24 N-linked (GlcNAc...) (Potential).
FT CARBOHYD       28 28 N-linked (GlcNAc...) (Potential).
FT CARBOHYD       183 183 N-linked (GlcNAc...) (Potential).
FT CONFLICT       192 192 F -> L (in Ref. 3).
SQ SEQUENCE       370 AA; 41895 MW; 20857F52A3929E48 CRC64;

Query Match          24.9%; Score 402; DB 1; Length 370;
Best Local Similarity 34.1%; Pred. No. 1.5e-22;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AYLGVLVLLGLNSLALWVFCRCMQQWTTETRIYMTNLAVADLCLLCTLPF-VLHSLR-- 81
DB 44 AVYVVFILGLITNSVLSVFCFRMKMRSETAIFTINLAVSDLLFVCTLPFKIFYNFNRH 103

QY 82 -DTSPTPLCOLSQGIYLTNRYSISLVTAIANDRYAVVRHPLRARGLSRPROAAVCAVL 140
DB 104 WPFQGT-LCKISGTAFLTNIYSGMLFLTCISVDRLAIVYFPRSTIRTRNSAIVCAGV 162

QY 141 WVLVIGSLVARMLGQIE-----GGFCFRSTRHNFNSMR--FPLLGFLYPLAVVVF 189
DB 163 WILVLSGGISASLSFTTNVNNATTCFEGFSKRVKTKYLSKITIFIEVVGFPIPLINVS 222

QY 190 CSLKVVYVTLAQRPPDVGQAEAT-RKAARMVWVANLLVFVVCFLPLHVLGTVRLAVGWNAC 248
DB 223 CSSVVLRTL--RKPAITLSQIGTNKKVLMITHMAVVFVCFVYNSVLFYALVRSQAI 280

QY 249 --ALLETIRRALY-ITSKLSANDCCLDACIYYMAKEQFQASALAVAPRAKAHKSQDSL 305
DB 281 TNCFLERPAKIMYPITLCLATLNCPCDFPIIYFTLESFQKSFVI-----NAHRMESLF 334

QY 306 VT 307
DB 335 KT 336

RESULT 7
Q6NSP5
ID Q6NSP5 PRELIMINARY; PRT; 370 AA.
AC Q6NSP5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE G protein-coupled receptor 23.
GN Name=GPR23;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RC TISSUE=PCR rescued clones;
RA Strausberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC069996; AAH69996.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045028; F:purinergic nucleotide receptor activity; G-. .; IEA.
DR GO; GO:004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR002188; P2Y5_purinocptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_HODOPSIN.
DR PRINTS; PR01067; P2Y5ORPHAN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE       370 AA; 41867 MW; 2AB4B3F5F43FFF83 CRC64;

Query Match          24.8%; Score 400; DB 2; Length 370;
Best Local Similarity 34.1%; Pred. No. 2.2e-22;
Matches 103; Conservative 59; Mismatches 112; Indels 28; Gaps 10;

QY 25 AYLGVLVLLGLNSLALWVFCRCMQQWTTETRIYMTNLAVADLCLLCTLPF-VLHSLR-- 81
DB 44 AVYVVFILGLITNSVLSVFCFRMKMRSETAIFTINLAVSDLLFVCTLPFKIFYNFNRH 103

QY 82 -DTSPTPLCOLSQGIYLTNRYSISLVTAIANDRYAVVRHPLRARGLSRPROAAVCAVL 140
DB 104 WPFQGT-LCKISGTAFLTNIYSGMLFLTCISVDRLAIVYFPRSTIRTRNSAIVCAGV 162

QY 141 WVLVIGSLVARMLGQIE-----GGFCFRSTRHNFNSMR--FPLLGFLYPLAVVVF 189
DB 163 WILVLSGGISASLSFTTNVNNATTCFEGFSKRVKTKYLSKITIFIEVVGFPIPLINVS 222

QY 190 CSLKVVYVTLAQRPPDVGQAEAT-RKAARMVWVANLLVFVVCFLPLHVLGTVRLAVGWNAC 248
DB 223 CSSVVLRTL--RKPAITLSQIGTNKKVLMITHMAVVFVCFVYNSVLFYALVRSQAI 280

QY 249 --ALLETIRRALY-ITSKLSANDCCLDACIYYMAKEQFQASALAVAPRAKAHKSQDSL 305
DB 281 TNCFLERPAKIMYPITLCLATLNCPCDFPIIYFTLESFQKSFVI-----NAHRMESLF 334

QY 306 VT 307
DB 335 KT 336

RESULT 8
Q6BKK1
ID Q6BKK1 PRELIMINARY; PRT; 370 AA.
AC Q6BKK1;
DT 01-WAR-2003 (TrEMBLrel. 23, Created)
DT 01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length
DE enriched library, clone: D130067B12 product: P2Y PURINOCCEPTOR 9, full
DE insert sequence.
GN Name=Gpr23;

```



OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxId=10090;  
 OX [1]\_SEQUENCE FROM N.A.  
 RP STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
 RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RX Carninci P., Hayashizaki Y.;  
 RA "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
 RA The FANTOM Consortium;  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujisake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer.";  
 RL Genome Res. 10:1757-1771(2000).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Inotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Taya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK051709; BAC34729.1; -;  
 DR MGD; MGI:1925384; Gpr23.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0045028; F:purinergic nucleotide receptor activity; G...; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodopsin.  
 DR InterPro; IPR002188; P2Y5\_purinocptor.  
 DR Pfam; PF00001; 7tm\_1; 1.

DR PRINTS; PR00237; GPCRHOOPS.N.  
 DR PRINTS; PR01067; P2Y5ORPHAN.  
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR\_F1.1; UNKNOWN\_1.  
 DR PROSITE; PS00262; G-PROTEIN RECEPTOR\_F1.2; 1.  
 SQ SEQUENCE 370 AA; 41956 MW; ABI26B42343456E1 CRC64;  
 Query Match 24.8%; Score 400; DB 2; Length 370;  
 Best Local Similarity 34.3%; Pred.No. 2.2e-22;  
 Matches 104; Conservative 59; Mismatches 112; Indels 28; Gaps 11;  
 QY 4 TYNTCGSSDLTWPPAIKLGfy-AYLGVLVLLGLLNSLWVFCRCMQQWTTETRIYVNL 62  
 DB 27 TNNTCIVDD-----SFKNLNGAVSVVFLGLIINSASLFFVCFRKMRSETAIFITNL 81  
 QY 63 AVADLCCLCTUPF-VLHSLR---DTSDDLPLCOLSGIYLTNRYMSISLTAIAVDYVAV 118  
 DB 82 ALSDLLFVCTLPFKIFYFNHRHWPFGDT-LCKISGTAFLNTIYGSMLFLTCISVDFLAI 140  
 QY 119 RHPLRARGLRSPROAAVCAVLWLVIGSLVARWLLGQe-----GGFCFRSTRHN 169  
 DB 141 VYPPRSRTIRTRNSAIVCAGVWILVINGGISASLFTTNVNNATTCPEGFSKRVKTY 200  
 QY 170 FNSMR--FPLLGfYLPVAVVFCSLKVVTAQAQRPPTDVQAEAT-RKAARVWVANLLVF 226  
 DB 201 LSKITIFIEVVGFIPLILNWCSSVVLRTL--RKPATLSQIGTNKKVLMITVMAVFP 258  
 QY 227 VVCFPLHVGLTVRLAVGNAC--ALLETRDALY-ITSKLSANDCCDLDAICYYNMAKFP 283  
 DB 259 VVCFVYNSVFLYALVRSQAITNCLERFAKIMYPITLCLATLNCDFPFYFYFTLESF 318  
 QY 284 QEA 286  
 DB 319 QKS 321  
 RESULT 9  
 Q8BLG2 PRELIMINARY; PRT; 370 AA.  
 AC Q8BLG2;  
 DT 01-MAR-2003 (TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Mus musculus 9.5 days embryo parthenogenote cDNA, RIKEN full-length  
 DE enriched library, clone:BI30055L15 product:P2Y PURINOCEPTOR 9, full  
 DE insert sequence.  
 GN Name=Gpr23;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;  
 RA The FANTOM Consortium;  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN [4]



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QY 32 VLGLLNSLALWVFC-----RMOQWTEPIYMTNLAVADLCILCTLPFVLHSLRDTSDTP 87
Db 32 VLGLLNSLALWVFC-----RMOQWTEPIYMTNLAVADLCILCTLPFVLHSLRDTSDTP 91
QY 88 -LCQLSQGIYLTNRYSISLVTAIVADRYAVRHPLRAGRLSPROAAAVCAVLVIV-1 145
Db 92 SLCTLVECLYFVSMYGSVFTICFISMDRELAIYPLVSHLSPRKIFGICCTIWLIVWT 151
QY 146 GSLVARWLLGIOEGCFRSTRHNFN-----SMRFPPL--LGFYLPVAVVFCSLKVTA 197
Db 152 GSPIYISFHGKVEKVMCF-----HNMSDDTWSAKVFPFLEVFGLPMLGFMGFCSSRSIHI 207
QY 198 LAQRPPTDVGQAEATKAA-RMVWANLVFVVCFLPHVGLTVRLAVGNW-----ACALLET 253
Db 208 LLGR--RDHTODWVOOKACIYSIASLAVFVVFSLPHVGLFGLFQLQFLVRNSFIVECRAKOS 265
QY 254 IRRALYITSKLSDANCCCLDAICYVMYMAKEFQ 284
Db 266 ISFFQLQSCFNVNCCLDVFCYFYVIKEFR 296

RESULT 11
ID Q8TDS4 PRELIMINARY; PRT; 363 AA.
AC Q8TDS4;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE G protein-coupled receptor HM74a (Seven transmembrane helix
DE receptor).
DE Name=GPCR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE FROM N.A.
RA Takeda S., Kadowaki S., Haga T., Takasue H., Mitaku S.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN 2;
RP SEQUENCE FROM N.A.
EX MEDLINE=2513958; PubMed=12522134; DOI=10.1074/jbc.M210695200;
RA Wise A., Foord S.M., Fraser N.J., Barnes A.A., Elshourbagy N.,
RA Eiler M., Ignar D.M., Murdock P.R., Steplewski K., Green A.,
RA Brown A.J., Dowell S.J., Szekeres P.G., Hassall D.G., Marshall F.H.,
RA Wilson S., Pike N.B.;
RT "Molecular identification of high and low affinity receptors for
RT nicotinic acid.";
RL J. Biol. Chem. 278:9869-9874 (2003).
RN 3;
RP SEQUENCE FROM N.A.
RA Elshourbagy N.A.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN 4;
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AB083632; BAB9345.1; -.
DR EMBL; AY148884; AAN71621.1; -.
DR EMBL; AB065876; BAC06094.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045028; F:purinergic nucleotide receptor activity, G-. .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR Rhodopsn.
DR InterPro; IPR002286; P2_purnocptor.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR01157; P2YPURNOCPTR.
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DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 363 AA; 41849 MW; C4B0EC9CCB81D56 CRC64;

Query Match      23.3%; Score 375.5; DB 2; Length 363;
Best Local Similarity 34.1%; Pred. No. 1.5e-207;
Matches 94; Conservative 48; Mismatches 107; Indels 27; Gaps 10;

QY 27 LGVLAVLGLLNSLALWVFCRMOQWTEPIYMTNLAVADLCILCTLPFVLHSL-----R 81
Db 34 LGLEIFGLGLGLALWIFCFHLKSKWSSRIFLFLNLAADFLLIICLPFLMDNYVRRWDW 93
QY 82 DTSDFPLQLSQGIYLTNRYSISLVTAIVADRYAVRHPLRAGRLSPROAAAVCAVLW 141
Db 94 KFGDTP-CRLMLFMLAMNRQSGIIFLTIVVADRYFVVRVPHHAKNISRTAAIISCLW 152
QY 142 VLIVIGSLV--ARWLLGIOEGG--FCFR--STRHNF--NSMRFPPLGFLYLPVAVVFCSLKV 194
Db 153 GITIGLTVHLLKKKMPIONGGANLCSFSICHTFQWHEAMP-LLEFFFLPLGLIILFCSARI 211
QY 195 VTALAQRPTDVGQAEATKKAARMVMWANLVFVVCFLPHVGLTVRLAVGNW-----NA 247
Db 212 IWSLRQ---QMDRHAKIKRAITFIMVVAIVFVICFLP---SVVVRIRIFWLLHTSGTQN 265
QY 248 CALLETIRRALYITSKLSDANCCCLDAICYVMYMAKEF 283
Db 266 CEVRSVDLAFFITLFTSYMNSMLDPVVVYFSSPSF 301

RESULT 12
P2Y5_CHICK
ID P2Y5_CHICK STANDARD; PRT; 308 AA.
AC P32250;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE P2Y purinoceptor 5 (P2Y5) (Purinergic receptor 5) (6H1).
GN Name=P2Y5;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=93329058; PubMed=8393036;
RA Kaplan M.H., Smith D.I., Sundick R.S.;
RT "Identification of a G protein coupled receptor induced in activated T
RT cells.";
RL J. Immunol. 151:628-636 (1993).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Induced in activated T-cells.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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or send an email to license@isb-sib.ch).

EMBL; L06109; AAS06587.1; -.
DR PIR; I50241; I50241.
DR HSP; P34996; 1DDD.
DR InterPro; IPR000276; GPCR Rhodopsn.
DR InterPro; IPR002188; P2Y5_purnocptor.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; GPCRHHODOPSN.
DR PROSITE; PS50237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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KW G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;  
 KW Transmembrane.  
 FT DOMAIN 1 16 Extracellular (Potential).  
 FT TRANSMEM 17 43 1 (Potential).  
 FT DOMAIN 44 52 Cytoplasmic (Potential).  
 FT TRANSMEM 53 76 2 (Potential).  
 FT DOMAIN 77 89 Extracellular (Potential).  
 FT TRANSMEM 90 109 3 (Potential).  
 FT DOMAIN 110 130 Cytoplasmic (Potential).  
 FT TRANSMEM 131 151 4 (Potential).  
 FT DOMAIN 152 178 Extracellular (Potential).  
 FT TRANSMEM 179 206 5 (Potential).  
 FT DOMAIN 207 224 Cytoplasmic (Potential).  
 FT TRANSMEM 225 250 6 (Potential).  
 FT DOMAIN 251 269 Extracellular (Potential).  
 FT TRANSMEM 270 289 7 (Potential).  
 FT DOMAIN 290 308 Cytoplasmic (Potential).  
 FT CARBOHYD 5 5 N-linked (GlcNAc..). (Potential).  
 FT LIPTD 281 281 S-palmitoyl cysteine (By similarity).  
 FT DISULFID 86 165 Potential.  
 SQ SEQUENCE 308 AA; 35597 MW; 4214E969633B6F7D CRC64;  
 Query Match 22.8%; Score 368.5; DB 1; Length 308;  
 Best Local Similarity 30.3%; Pred. No. 4.5e-20;  
 Matches 91; Conservative 64; Mismatches 102; Indels 43; Gaps 10;  
 QY 10 SSDLTWPAPKAGFY-AYLGVLVLLGLLNSLALWVFCRMOQWETETRIYMTNLAVADLC 68  
 Db 3 SSNCSTEDSFYKTLGCVSMFVLGLIANCAVIAFTFLKVRNETTMYMLNLAISDLL 62  
 QY 69 LACTLPFLVLSLSDTDP- ---LQLSQGIYLTNRYMSISLVTAADVAVVRHPLRA 124  
 Db 63 FVFTLPFRRIYF-VRNWPFQGVLCISVTLYTNMYGSLFTLCISVDRLAIVHPFRS 121  
 QY 125 RGLSPRQAAACAVLWLVLI-GSLVARWLLGTOEGGFCFST-RHNFNSMR- ----FP- 176  
 Db 122 KTLTKRNARIVCVAWITVLASTPASP- ----FQSTNRQNTEQRTCFENPPE 171  
 QY 177 -----LLGYPPLAVVVFCSLKVVTALAQRPTDVGOABATKARWVA 221  
 Db 172 STWKTYLSRIVIFIEIVGFFIPLINVTCTWVLRTL-NKPLTLRNKLSKKVLMKIPV 230  
 QY 222 NLLAVFVCFPLPHVGL- ---TVRLAVGWNAALLETIRRALYITSKLSDANCCLDACYYY 278  
 Db 231 HLIVFCFCFVPNTILILYSMLRTQTWNCVSVTAVRTVYPTVLCIAVSNCCFDPIVYF 290  
 RESULT 13  
 G09B\_HUMAN  
 ID G09B\_HUMAN STANDARD; PRT; 387 AA.  
 AC P49019;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Probable G protein-coupled receptor GPR109B (G protein-coupled receptor HM74).  
 GN Name=GPR109B; Synonyms=HM74;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Monocytes;  
 RX MEDLINE=94092629; PubMed=7505609;  
 RA Nomura H., Nielsen B.W., Matsushima K.;  
 RT "Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte chemotactic peptide receptors.";  
 RL Int. Immunol. 5:1239-1249(1993).  
 CC -!- FUNCTION: Orphan receptor.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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 DR EMBL; D10923; BAA01721.1; -.  
 DR PIR; I69202; I69202.  
 DR HSSP; P34996; IDDD.  
 DR Genew; HGNC:16824; GPR109B.  
 DR MIM; 606039; -.  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.  
 DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. . .; TAS.  
 DR InterPro; IPR000276; GPCR Rhodpsn.  
 DR InterPro; IPR002286; P2\_purinocptor.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PR00237; GPCRHHODOPSN.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane.  
 FT DOMAIN 1 28 Extracellular (Potential).  
 FT TRANSMEM 29 50 1 (Potential).  
 FT DOMAIN 51 63 Cytoplasmic (Potential).  
 FT TRANSMEM 64 85 2 (Potential).  
 FT DOMAIN 86 102 Extracellular (Potential).  
 FT TRANSMEM 103 123 3 (Potential).  
 FT DOMAIN 124 142 Cytoplasmic (Potential).  
 FT TRANSMEM 143 163 4 (Potential).  
 FT DOMAIN 164 194 Extracellular (Potential).  
 FT TRANSMEM 195 209 5 (Potential).  
 FT DOMAIN 210 236 Cytoplasmic (Potential).  
 FT TRANSMEM 237 256 6 (Potential).  
 FT DOMAIN 257 273 Extracellular (Potential).  
 FT TRANSMEM 274 298 7 (Potential).  
 FT DOMAIN 299 387 Cytoplasmic (Potential).  
 FT DISULFID 100 177 By similarity.  
 SQ SEQUENCE 387 AA; 44481 MW; C244F562C2343647 CRC64;  
 Query Match 22.8%; Score 368.5; DB 1; Length 387;  
 Best Local Similarity 34.3%; Pred. No. 5.5e-20;  
 Matches 95; Conservative 48; Mismatches 105; Indels 29; Gaps 11;  
 QY 27 LGVLVLGILLNSLALWVFCRMOQWETETRIYMTNLAVADLCCLTLPVL- ----HSLR 81  
 Db 34 LGLEIFGLGLGLALWIFCFHLKSWKSRIPLFNLAVALADFLLIITCLPFVMDYVYRRSDW 93  
 QY 82 DTSPTPLCQLSQGIYLTNRYMSISLVTAADVAVVRHPLRARGLSRQAAAVCAVLW 141  
 Db 94 NFGDIP-CRLVLFMFAMNRQSGIIFTVVADVRYFRVPHPHALNKISNWTAAISCLW 152  
 QY 142 VLIVIG- ---SLVARWLLGIQEG--GFCFR-STRHNF--NSMRPPLGLFYLPVLAVVVFCSLK 193  
 Db 153 GITVGLTVHLLKKLL-IQNGPANVCISFSICTFRWHEAMF-LLEFLPLGLILFCSAR 210  
 QY 194 VVTLAQRPPTDVGOABATKARWVANLLVFVCFPLPHVGLTVRLAVGW- ----N 246  
 Db 211 IIVSLRQR- ---QMDRHAKIKRAITFIMVVAIVFVICFLP- ---SVVVRIRIFMLLHTSGTQ 264  
 QY 247 ACALLETIRRALYITSKLSDANCCLDACYYYMAKEF 283  
 Db 265 NCEVYRVDLAFITLSTFYTNMSMLDPPVYVYSSPSF 301  
 RESULT 14  
 Q8NGE4  
 ID Q8NGE4 PRELIMINARY; PRT; 387 AA.  
 AC Q8NGE4;  
 DT 01-OCT-2002 (TremBLrel. 22, Created)  
 DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 23, 2005, 11:17:30 ; Search time 19.5 Seconds  
(without alignments)  
1182.901 Million cell updates/sec

Title: US-10-083-168-85  
Perfect score: 1615  
Sequence: 1 MNGYNTCGSSDLTPWPAIK.....AVAPRAKAKSODSLCVTLA 309

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
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2: /cgn2\_6/ptodata/1/iaa/5B COMB.pap:\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pap:\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pap:\*  
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6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1609	99.6	309	3	US-09-422-869-20
2	401	24.8	370	3	US-08-781-250-2
3	374.5	23.2	387	4	US-09-170-496D-222
4	369.5	22.9	387	4	US-09-170-496D-108
5	369.5	22.9	387	4	US-09-944-807-21
6	360.5	22.3	344	2	US-08-467-948A-8
7	360.5	22.3	344	3	US-08-467-947A-8
8	359.5	22.3	302	2	US-08-467-948A-30
9	359.5	22.3	302	3	US-08-467-947A-30
10	328.5	20.3	377	4	US-09-745-842-17
11	327.5	20.3	374	4	US-09-710B-3
12	320	19.8	362	3	US-08-513-974B-374
13	318.5	19.7	346	4	US-09-585-876-2
14	317.5	19.7	391	4	US-09-826-509-463
15	316	19.6	374	4	US-09-745-842-15
16	315.5	19.5	365	4	US-09-745-842-16
17	315.5	19.5	365	4	US-09-077-173D-2
18	315	19.5	373	3	US-08-513-974B-373
19	311.5	19.3	354	4	US-09-364-425B-60
20	311.5	19.3	362	4	US-09-170-496D-4
21	311.5	19.3	368	4	US-08-148-708-2
22	310.5	19.2	358	4	US-09-170-496D-186
23	310	19.2	342	3	US-09-826-509-555
24	309	19.1	342	3	US-08-988-876-9
25	307.5	19.0	362	4	US-09-170-496D-166
26	306.5	19.0	375	1	US-08-442-134A-2
27	306.5	19.0	375	1	US-08-444-581B-2

28	306.5	19.0	375	1	US-08-446-088A-2	Sequence 2, Appli
29	306.5	19.0	375	2	US-08-553-524A-3	Sequence 3, Appli
30	306.5	19.0	375	3	US-08-749-707-3	Sequence 3, Appli
31	306.5	19.0	375	4	US-09-947-922-3	Sequence 3, Appli
32	305.5	18.9	327	3	US-08-513-974B-372	Sequence 372, App
33	305.5	18.9	358	3	US-09-041-545-2	Sequence 2, Appli
34	305.5	18.9	358	3	US-09-327-925-2	Sequence 2, Appli
35	305	18.9	339	4	US-09-170-496D-182	Sequence 182, App
36	303	18.8	342	4	US-09-054-272-2	Sequence 2, Appli
37	302	18.7	326	1	US-08-118-270-39	Sequence 39, Appli
38	302	18.7	326	5	PCT-US93-08528-39	Sequence 39, Appli
39	301	18.6	328	3	US-08-513-974B-39	Sequence 39, Appli
40	301	18.6	328	3	US-08-513-974B-371	Sequence 371, App
41	301	18.6	328	4	US-09-461-436B-39	Sequence 39, Appli
42	300.5	18.6	93	3	US-09-724-864-61	Sequence 61, Appli
43	300.5	18.6	373	2	US-08-559-524A-4	Sequence 4, Appli
44	300.5	18.6	373	3	US-08-749-707-4	Sequence 4, Appli
45	300.5	18.6	373	4	US-09-947-922-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1  
US-09-422-869-20  
; Sequence 20, Application US/09422869  
; Patent No. 6235481  
; GENERAL INFORMATION:  
; APPLICANT: POLONSKY, KENNETH S.  
; APPLICANT: HORIKAWA, YUKIO  
; APPLICANT: ODA, NAOHISA  
; APPLICANT: COX, NANCY J.  
; APPLICANT: ZHEENAN, SEAMUS  
; APPLICANT: ZHOU, YUN-PING  
; APPLICANT: OTANI, KENICHI  
; APPLICANT: HANIS, CRAIG I.  
; APPLICANT: BELL, GRAEME I.  
; TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES  
; FILE REFERENCE: ARCD:307  
; CURRENT APPLICATION NUMBER: US/09/422,869  
; CURRENT FILING DATE: 1999-10-21  
; EARLIER APPLICATION NUMBER: 60/134,175  
; EARLIER FILING DATE: 1999-05-13  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Human  
US-09-422-869-20

Query Match	99.6%	Score 1609;	DB 3;	Length 309;
Best Local Similarity	99.7%	Pred. No. 4.5e-132;	Mismatches 1;	Indels 0;
Matches 308;	Conservative 0;			Gaps 0;
QY	1	MNGYNTCGSSDLTPWPAIKLGFYAYLGVLLVGLLNSLALWVFCRCRQQTETRIYMT	60	
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QY	61	NLAVADLCLLCTLPVLHSLRDTSTPLCOLSQGLYLTNRNYSISLVTAIADRVYVVRH	120	
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QY	121	PIRAGRLSPQAAACAVLWLVLSLVARWLLGIQEGGFCFRTRNFNSMRPFLIGF	180	
Db	121	PIRAGRLSPQAAACAVLWLVLSLVARWLLGIQEGGFCFRTRNFNSMRPFLIGF	180	
QY	181	YPLVAVVFCSLKVVVTALAQRPPTDVQGAETRAKRAKRWANLLVYVVCFLFLHVLTVR	240	
Db	181	YPLVAVVFCSLKVVVTALAQRPPTDVQGAETRAKRAKRWANLLVYVVCFLFLHVLTVR	240	
QY	241	LAVGWNCALLETTRRALLYITISKUSDANCCLDIAICYWMAKEFQASALAVAPRAKHS	300	

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Db      241  LAVGNWACALLETIRRALYITSKLSDANCCLDAICYYWAKEFQASALAVAPRAKAHKS 300

QY      301  QDSLVCVTLA 309
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Db      301  QDSLVCVTLA 309

RESULT 2
US-08-781-250-2
; Sequence 2, Application US/08781250
; Patent No. 6010877
; GENERAL INFORMATION:
; APPLICANT: Sathe, Ganesh
; APPLICANT: Van Horn, Stephanie
; APPLICANT: Bergsma, Derk
; APPLICANT: Mao, Joyce Yue
; TITLE OF INVENTION: CDNA CLONE HERCS41 THAT ENCODES A NOVEL 7-TRANSMEMBRAN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,250
; FILING DATE: 10-JAN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: William T. Han,
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: ATGS0043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-4060
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 370 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-781-250-2

Query Match 24.8%; Score 401; DB 3; Length 370;
Best Local Similarity 34.1%; Pred. No. 3.9e-27;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY      25  AYLGVLLVTLGLLNSIALWVFCRCMQQWETRIYMTNLAVALDCLLCTLP-VLHSLR-- 81
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         | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      44  AVYSVVFILGLITNSVSLVFCFPMQMRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103

QY      82  -DTSDFPLCOLSOGIVLTNRYNSISLVTALAVDRYVAVRHPLRAGLSRPROAAACAVL 140
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         || ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |
Db      104  WPFQDGT-LCKISTGTAFTNIYSGMLFATCISVDRLFAIVYPPRSRTIITRRNSAIVCAGV 162
         || ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |
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QY      141  WLVLVGLSVAWRLLGIQE-----GGFCFRSTRHNFSNR--FPLLIGFYLPVAVVVF 189
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         || ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |
         || ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |
Db      163  WILVLSGIGISALFESTIVNNVNTTCFEGFSKEVWKYLSKITIFIEVVGFIIPLILNV 222

QY      190  CSKLKVTVALLAQRPTDVQGAET-RKAKRMVWANLLVFCVFLPHVGLTVSLAVGNAC 248
         || ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |
         || ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |
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Db      223  CSSVVLRTL--RKPATLSQIGTNKKVKLKMIVHMAVFCVFCFVNSVLFYALVRSQAI 280
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; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-170-496D-108

Query Match 22.9%; Score 369.5; DB 4; Length 387;  
Best Local Similarity 35.0%; Pred. No. 2.2e-24;  
Matches 98; Conservative 45; Mismatches 102; Indels 35; Gaps 12;

QY 27 LGVLVLGLLNSLALWVFCRCMQWETRIYMTNLAVADLCCLTLPVL-----HSLR 81  
DB 34 LGLEIFGLGLNLGLALWIFCPHLKSKWSRIEFLNLAVADFLIICLPFVMDYVYRRSDW 93  
QY 82 DTSDFPLCQLSGIYLTNRYSISLVTAIVDRYVAVRHPLRARGLSRQAAAVCAVLW 141  
DB 94 NFGDIP-CRLVLFMFAMNRQSGIIFLTVAVDYRFRVPHPHALNKISNWTAAIISCLW 152  
QY 142 VLIVG---SLVARWLLGIQEG--GFCFR-STRHNF--NSMRPFLGLFYLPLAVVVFCSLK 193  
DB 153 GITVGLTVHLLKKLL-IQNGPANVCISFSICHTFRWHEAMP-LLEFLLPLGIIIFCSAR 210  
QY 194 VVTAQAQRPPTDVGQAETRAKAKR---MVANLLVFVVCFLPLHVLGTLVRLAVGW----- 245  
DB 211 IWSLRQR-----QMDRHAQIKRAITFTMVVAIVFVICFLP---SVVVRIRIFWLLHTS 261  
QY 246 --NACALLETTIRALYITSKSDANCCCLDAICYYYMAKEF 283  
DB 262 GTQNCVYRVDLAFITLSFTYMNMLDPVVYFSSPSF 301

RESULT 5  
US-09-944-807-21  
; Sequence 21, Application US/09944807  
; Patent No. 6773895  
; GENERAL INFORMATION:  
; APPLICANT: Boehringer Ingelheim Pharma KG  
; TITLE OF INVENTION: Method for identifying substances which positively  
; TITLE OF INVENTION: influence inflammatory conditions of chronic  
; TITLE OF INVENTION: inflammatory airway diseases  
; FILE REFERENCE: 082 00n  
; CURRENT APPLICATION NUMBER: US/09/944,807  
; CURRENT FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: UK 0021484.1  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 387  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-944-807-21

Query Match 22.9%; Score 369.5; DB 4; Length 387;  
Best Local Similarity 35.0%; Pred. No. 2.2e-24;  
Matches 98; Conservative 45; Mismatches 102; Indels 35; Gaps 12;

QY 27 LGVLVLGLLNSLALWVFCRCMQWETRIYMTNLAVADLCCLTLPVL-----HSLR 81  
DB 34 LGLEIFGLGLNLGLALWIFCPHLKSKWSRIEFLNLAVADFLIICLPFVMDYVYRRSDW 93  
QY 82 DTSDFPLCQLSGIYLTNRYSISLVTAIVDRYVAVRHPLRARGLSRQAAAVCAVLW 141  
DB 94 NFGDIP-CRLVLFMFAMNRQSGIIFLTVAVDYRFRVPHPHALNKISNWTAAIISCLW 152  
QY 142 VLIVG---SLVARWLLGIQEG--GFCFR-STRHNF--NSMRPFLGLFYLPLAVVVFCSLK 193  
DB 153 GITVGLTVHLLKKLL-IQNGPANVCISFSICHTFRWHEAMP-LLEFLLPLGIIIFCSAR 210  
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DB 211 IWSLRQR-----QMDRHAQIKRAITFTMVVAIVFVICFLP---SVVVRIRIFWLLHTS 261  
QY 246 --NACALLETTIRALYITSKSDANCCCLDAICYYYMAKEF 283

DB 262 GTQNCVYRVDLAFITLSFTYMNMLDPVVYFSSPSF 301

RESULT 6  
US-08-467-948A-8  
; Sequence 8, Application US/08467948A  
; Patent No. 5998164  
; GENERAL INFORMATION:  
; APPLICANT: LI, YI  
; APPLICANT: CAO, LIANG  
; APPLICANT: NI, JIAN  
; APPLICANT: GENTZ, REINER  
; APPLICANT: BUILT, CAROL J.  
; APPLICANT: SUTTON III, GRANGER G.  
; APPLICANT: ROSEN, CRAIG A.  
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein  
; TITLE OF INVENTION: Coupled Receptor GPR2  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVE., NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467,948A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04079  
; FILING DATE: 30-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 344 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-467-948A-8

Query Match 22.3%; Score 360.5; DB 2; Length 344;  
Best Local Similarity 29.2%; Pred. No. 1.2e-23;  
Matches 90; Conservative 68; Mismatches 107; Indels 43; Gaps 10;

QY 10 SSDLTWPPAIIKLGFYAYL-GVLLVGLLNSLALWVFCRCMQWETRIYMTNLAVADLC 68  
DB 6 SSHCFYNDSEKTYLYGCMFVMVGLISNCVAIYFICVLKVRNETTYMINLAMSDDL 65  
QY 69 LLCTLPFVLHSLURDSDTP-----LCQLSGIYLTNRYSISLVTAIVDRYVAVRHPLRA 124  
DB 66 FVFTLPFIRIFYP-TTRNWPFGDLLCKISVMLFTNMYGSIILFTLCISVDRLAIVYPPKS 124  
QY 125 RGLSPROAAVCAVLWLVVI-GSLVARWLLGIQEGG-----FCFRSTRHNFNSMRFP-- 176  
DB 125 KTLRTRKNAKIVCTGVMLTVIGGSAPAVFVQSTHSGQGNNAEACFEN-----FPEA 175  
QY 177 -----LLGFYPLAVVVFCSLKVVVTALAQRPPTDVGQAETRAKAKMVA 221  
DB 176 TWKTYLSRIVFIEIVGFIFPLINVTCTSSMVLKTLTK--PVTLSRSKINKTKVLMIV 233  
QY 222 NLLVFVVCFLPLHVLGTLVRLAVGWNA---CALLETIRALYITSKSDANCCCLDAICYYY 278

Db 234 HLIIFCFVFPYNINLILYSLVRTQTQFVNCVVAARVTMYPTITLCIAVSNCCFDPVIVYF 293  
QY 279 MAKEFOEA 286  
Db 294 TSDTIQNS 301  
RESULT 7  
US-08-467-947A-8  
; Sequence 8, Application US/08467947A  
; Patent No. 6090575  
; GENERAL INFORMATION:  
; APPLICANT: LI, YI  
; APPLICANT: CAO, LIANG  
; APPLICANT: NI, JIAN  
; APPLICANT: GENTZ, REINER  
; APPLICANT: BULT, CAROL J.  
; APPLICANT: SUTTON III, GRANGER G.  
; APPLICANT: ROSEN, CRAIG A.  
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein  
; TITLE OF INVENTION: Coupled Receptor GPR1  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVE., NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467,947A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04079  
; FILING DATE: 30-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 344 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-467-947A-8  
Query Match 22.3%; Score 360.5; DB 3; Length 344;  
Best Local Similarity 29.2%; Pred. No. 1.2e-23;  
Matches 90; Conservative 68; Mismatches 107; Indels 43; Gaps 10;  
QY 10 SSDLTWPPAIKLGFIAYL-GVLLVLGLLNSLALWFCRCMQQWTEIRIYMTNLAVADLC 68  
Db 6 SSHCFYNDSEFKYTLGCMFSWVFLGLNSLALWFCRCMQQWTEIRIYMTNLAVADLC 65  
QY 69 LLCTLPFVLHSLRDTSDTP----LCQLSQGIYLTNRYSISLVTAIVADRYAVVRHPLRA 124  
Db 66 FVTLPRFRIEYF-TTRNWFPGDLLCKISWMLFTYNNYGSILFELTCLISVDRFLAIVYFFKS 124  
QY 125 RGLRSQRAAAVCAVLWLVI-GSLVARMLLGIQEGG-----FCFRSTRHNFNSMRFP-- 176  
Db 125 KTI-RTKRNAKIVCTGWLTAVIGSGAPAVFVQSTHSQGNNAEACFEN-----FPBA 175

QY 177 -----LLGFYPLAVVVFGLSKVVTALAQRPPTDVQGAETR-KAKRMVMA 221  
Db 176 TKTYLSRIVFIEIVGFIFLILNVTCTSSWVLTITK--PVTLSRSKINKTKVKMIFV 233  
QY 222 NLLVFWCFLPLHVLGTLVRLAVGNA---CALLETIRALYITSKLSDANCCLDICYY 278  
Db 234 HLIIFCFVFPYNINLILYSLVRTQTQFVNCVVAARVTMYPTITLCIAVSNCCFDPVIVYF 293  
QY 279 MAKEFOEA 286  
Db 294 TSDTIQNS 301  
RESULT 8  
US-08-467-948A-30  
; Sequence 30, Application US/08467948A  
; Patent No. 5998164  
; GENERAL INFORMATION:  
; APPLICANT: LI, YI  
; APPLICANT: CAO, LIANG  
; APPLICANT: NI, JIAN  
; APPLICANT: GENTZ, REINER  
; APPLICANT: BULT, CAROL J.  
; APPLICANT: SUTTON III, GRANGER G.  
; APPLICANT: ROSEN, CRAIG A.  
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein  
; TITLE OF INVENTION: Coupled Receptor GPR2  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVE., NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467,948A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04079  
; FILING DATE: 30-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 302 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide  
US-08-467-948A-30  
Query Match 22.3%; Score 359.5; DB 2; Length 302;  
Best Local Similarity 30.0%; Pred. No. 1.3e-23;  
Matches 90; Conservative 64; Mismatches 103; Indels 43; Gaps 10;  
QY 10 SSDLTWPPAIKLGFIAYLGVLLVLGLLNSLALWFCRCMQQWTEIRIYMTNLAVADLC 68  
Db 1 SSSCTEDSEFKYTLGCVFSWVFLGLNCAVIAIYFTTLKVRNFTTYTMLAISDLL 60  
QY 69 LLCTLPFVLHSLRDTSDTP----LCQLSQGIYLTNRYSISLVTAIVADRYAVVRHPLRA 124

Db 61 FVFTLPERIYYF-VVRNMPFGDVLCKISVTLFTYTNMYGSILFLTCISVDRFLAIVHPERS 119  
QY 125 RGLRSPROAAACAVLWLVVI-GSLVARWLLGIQGGFCFRST-RHNFNSMR-----PP- 176  
Db 120 KTLRTKRNARIVCVAVWITVLGSPASF-----FQSTNRQNNTEQRTCPENFPE 169  
QY 177 -----LLGFYPLAVVVFCSLKVVTALAQRPPTDVGOAEATRKAKRWYWA 221  
Db 170 STWKTYLSRIVIFIBIVGFIFLIILNVCTSWLRTL-NKPLTLSENKLSKKVKLKMIFV 228  
QY 222 NLLVFWVCFPLHVLGL---TVRLAVGWNACALLETIRRALYITSKLSANDCCCLDAICY 278  
Db 229 HLIVFCFCFVPYNTILYLSMRQTWNCVSVTAVRTMYPTVTLCLAVSNCCCFDPIVYVF 288

## RESULT 9

US-08-467-947A-30  
; Sequence 30, Application US/08467947A  
; Patent No. 6090575  
; GENERAL INFORMATION:  
; APPLICANT: LI, YI  
; APPLICANT: CAO, LIANG  
; APPLICANT: NI, JIAN  
; APPLICANT: GENTZ, REINER  
; APPLICANT: BULT, CAROL J.  
; APPLICANT: SUTTON III, GRANGER G.  
; APPLICANT: ROSEN, CRAIG A.  
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein  
; TITLE OF INVENTION: Coupled Receptor GPR1  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 NEW YORK AVE., NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467,947A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/04079  
; FILING DATE: 30-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: STEFFE, ERIC K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 302 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide

US-08-467-947A-30

Query Match 22.3%; Score 359.5; DB 3; Length 302;  
Best Local Similarity 30.0%; Pred. No. 1.3e-23;  
Matches 90; Conservative 64; Mismatches 103; Indels 43; Gaps 10;

QY 10 SSDLTWPPAIGLGFY-AVLGVLVLLGLLNSLALWVFCRCMQQTETRIYMTNLAVADLC 68  
Db 1 SNNCTSDSFKTYLGYCVFWMVFLGLIANCVAIYIFTLKVRNETTITMLMLAISDLL 60

QY 69 LLCTLPFVLHSLRDTSDTP-----LCQLSQGIYLTNRVMSISLVTALAVDRVYVAVRPLRA 124  
Db 61 FVFTLPERIYYF-VVRNMPFGDVLCKISVTLFTYTNMYGSILFLTCISVDRFLAIVHPERS 119  
QY 125 RGLRSPROAAACAVLWLVVI-GSLVARWLLGIQGGFCFRST-RHNFNSMR-----PP- 176  
Db 120 KTLRTKRNARIVCVAVWITVLGSPASF-----FQSTNRQNNTEQRTCPENFPE 169  
QY 177 -----LLGFYPLAVVVFCSLKVVTALAQRPPTDVGOAEATRKAKRWYWA 221  
Db 170 STWKTYLSRIVIFIBIVGFIFLIILNVCTSWLRTL-NKPLTLSENKLSKKVKLKMIFV 228  
QY 222 NLLVFWVCFPLHVLGL---TVRLAVGWNACALLETIRRALYITSKLSANDCCCLDAICY 278  
Db 229 HLIVFCFCFVPYNTILYLSMRQTWNCVSVTAVRTMYPTVTLCLAVSNCCCFDPIVYVF 288

## RESULT 10

US-09-745-842-17  
; Sequence 17, Application US/09745842  
; Patent No. 6762029  
; GENERAL INFORMATION:  
; APPLICANT: Conley, Pamela B.  
; APPLICANT: Jantzen, Hans-Michael  
; APPLICANT: Ramakrishnan-DuBridge, Vanitha  
; APPLICANT: Jullius, David  
; APPLICANT: Hollopeter, Gunter  
; APPLICANT: COR Therapeutics, Inc.  
; TITLE OF INVENTION: P2Y12 Receptor  
; FILE REFERENCE: 44481-5053-US  
; CURRENT APPLICATION NUMBER: US/09/745,842  
; CURRENT FILING DATE: 2000-12-26  
; PRIOR APPLICATION NUMBER: US 60/171,622  
; PRIOR FILING DATE: 1999-12-23  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 377  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: P2Y2 purinergic receptor; p2ur  
US-09-745-842-17

Query Match 20.3%; Score 328.5; DB 4; Length 377;  
Best Local Similarity 33.1%; Pred. No. 7.8e-21;  
Matches 90; Conservative 47; Mismatches 108; Indels 27; Gaps 8;

QY 28 GVLVLGLLNSLALWVFCRCMQQTETRIYMTNLAVADLCCLTLPFVLHSLRDTSDTP 87  
Db 41 GVVCVLGLCLNAVALYIFLCRLKTNWASTTYMFHLAVSDALYAAASLPLLVYYYARGDHP 100  
QY 88 ---LCQLSQGIYLTNRVMSISLVTALAVDRVYVAVRPLRGLRSPROAAACAVLWVL 143  
Db 101 FSTVLCKLVRFLFTYTNLYCSILFLTCISVHRCIGVLRPLRSURWGRYARRVAGAVWL 160  
QY 144 VIG--SLVARWLLGIQGGFCFRSTRN-----FNSMRFPGLGFLPLAVVYVF 189  
Db 161 VLACQAPVLYFVTTTSARG--RVTCSDTSAPELFSRFVAYSSVLMGLL-FAVPPAVILV 216  
QY 190 CSLKVVVTALAQRP--TDVGQAEATRKAKRWYWANLLVFWVCFPLHVLGLTVRLAVGM-- 245  
Db 217 CVVLMARELL-KPAYGTSGGLPRAKRSVRTIAVVLAVFALCFLPFHVTRTLTYSPRSILD 275  
QY 246 NACALLETIRRALYITSKLSANDCCCLDAICY 277  
Db 276 LSCHTLNAINWAYKVTRPLASANSCLDPVLYF 307

## RESULT 11

US-09-102-710B-3  
; Sequence 3, Application US/09102710B  
; Patent No. 6479630

```
; GENERAL INFORMATION:
; APPLICANT: Coleman, Roger
; APPLICANT: Au-Young, Janice
; APPLICANT: Stuart, Susan G.
; TITLE OF INVENTION: A NOVEL HUMAN PURINERGIC P2U RECEPTOR
; FILE REFERENCE: PF-0038-1 DIV
; CURRENT APPLICATION NUMBER: US/09/102,710B
; CURRENT FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: RNU09402
US-09-102-710B-3

Query Match      20.3%; Score 327.5; DB 4; Length 374;
Best Local Similarity 29.2%; Pred. No. 9.4e-21;
Matches 99; Conservative 54; Mismatches 127; Indels 59; Gaps 10;

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Db  9  NSTINGTWGD-----ELGKCRPNEDFKYVLPVSGVGVVGLCLNVVALYFLCR 61

QY  49  MOQWETRIYMTNLAVADCLCTLPFVLHSLRDTSDTP---LCQLSQGIYLTNRYMSI 104
Db  62  LKTNASTYMFHLAVSDSLYAASLPLLVVYVYAGQDHPFSTVLCVLFVFTNLYCSI 121

QY  105  SLVTAIVDRYVAVRHPLRARGLRSPROAAVCAVLWLVIGS-----LVARWLLGTQE 158
Db  122  LFLTCTISVHSLGVLRLSLRWGHARYARRVAAVVMVLVACQTPVLYFVFTTSVRGT-- 179

QY  159  GGFCEPSTRHN-----FNSMRPFLGFLYPLAVVVFCSLKVVYALAQRPPTDV 206
Db  180  -----RITCHDTSDELFSHFVAYSSVMGLL-FAVPSIILVCYVMARLLKPAYGTT 233

QY  207  GOAEATRKAKRMVWNLVVFVVCFLPLHVLGLTVRLAVGW--NACALLETRALYITSKL 264
Db  234  GLPRAKKSVRTIALVLAVFALCFPLFHVTRTLVYFSRSLDLSCHTNAINMAYKITRPL 293

QY  265  SPANCCLDIAICYY-----NAKEQEQEASALAVAPRAK 296
Db  294  ASANSCLDPVLYFLAGQRLVRFARDAKAPATEPTPSQAR 332

RESULT 12
US-08-513-974B-374
; Sequence 374, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhiro
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: D'KE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-057186
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-007177
; FILING DATE: 20-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-326611
; FILING DATE: 28-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-270017
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236357
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236356
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189274
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189273
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 45753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 374:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 362 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-513-974B-374

Query Match      19.8%; Score 320; DB 3; Length 362;
Best Local Similarity 28.2%; Pred. No. 4.1e-20;
Matches 96; Conservative 64; Mismatches 133; Indels 48; Gaps 12;

QY  1  MNGTY-----NTCGSSDLTWPAPKLGFP-YAYLGVLLVL----GLLNSLALWV 44
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QY  45  FCRMQQWETRIYMTNLAVADCLCTLPFVLHSLRDTSD----TFLCQLSQGIYLTNR 100
Db  65  FVFHMRPMSGISVYMFNLALADFLVYLTLPALIFYFYFNKTDWIFGDMCKLQRFIFHVL 124

QY  101  YMSISIVTAIVDRYVAVRHPLRARGLRSPROAAVCAVLWLVIGSLVARWL----LGI 156
Db  125  YGSILFLTCTISVHRYTGVVHPLKSLGRKKKAAVYVSSIVWALVW-AVTAPILFYSGIGV 183

QY  157  QEGG--FCFRSTRHNF-----NSMRPFLGFLYPLAVVVFCSLKVVYALAQRPPTDVQ 208
Db  184  RRNKTITCYDTTADAYLRSYFVYSMTCTVFMFCIPFIVILGCVGLIVKALIKYK---DLON 240
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; SOFTWARE: FASTANALYSE v1.2.1
; SEQ ID NO 15
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Meleagris gallopavo
; FEATURE:
; OTHER INFORMATION: Turkey P2Y nucleotide receptor; tp2ynovel
US-09-745-842-15

Query Match          19.6%; Score 316; DB 4; Length 374;
Best Local Similarity 27.8%; Pred. NO. 9.4e-20;
Matches 80; Conservative 58; Mismatches 130; Indels

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 23, 2005, 11:25:32 ; Search time 55 Seconds  
(without alignments)  
1879.324 Million cell updates/sec

Title: US-10-083-168-85

Perfect score: 1615

Sequence: 1 MNGYNTCGSSDLTWPPAIAK.....AVAPRAKAKHSQDSLCTVLA 309

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
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- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1609	99.6	309	9	US-09-768-877-20
2	1609	99.6	309	14	US-10-225-567A-492
3	1609	99.6	309	17	US-10-696-639-44
4	1597	98.9	309	14	US-10-157-031-351
5	401	24.8	370	10	US-09-964-821B-11
6	401	24.8	370	14	US-10-081-810-44
7	401	24.8	370	14	US-10-225-567A-225
8	401	24.8	370	14	US-10-024-298A-176
9	401	24.8	370	14	US-10-042-211A-176
10	401	24.8	370	14	US-10-268-332-11
11	401	24.8	370	15	US-10-617-217A-176
12	401	24.8	370	17	US-10-753-267-86
13	400	24.8	370	10	US-09-964-821B-10

14	400	24.8	370	14	US-10-268-332-10	Sequence 10, Appl
15	391	24.2	370	14	US-10-024-298A-174	Sequence 174, App
16	391	24.2	370	14	US-10-042-211A-174	Sequence 174, App
17	391	24.2	370	15	US-10-617-217A-174	Sequence 174, App
18	382.5	23.7	363	16	US-10-314-048A-159	Sequence 159, App
19	382.5	23.7	363	16	US-10-897-815-159	Sequence 159, App
20	377.5	23.4	363	10	US-09-910-334-16	Sequence 16, Appl
21	377.5	23.4	363	15	US-10-619-141-16	Sequence 16, Appl
22	376.5	23.3	363	14	US-10-321-807-36	Sequence 36, Appl
23	376.5	23.3	363	15	US-10-295-027-226	Sequence 226, App
24	376.5	23.3	363	15	US-10-292-798-668	Sequence 668, App
25	376.5	23.3	363	16	US-10-321-807-36	Sequence 36, Appl
26	376.5	23.3	363	16	US-10-314-048A-36	Sequence 36, Appl
27	376.5	23.3	363	16	US-10-897-815-36	Sequence 766, App
28	376.5	23.3	364	14	US-10-017-161-766	Sequence 808, App
29	376.5	23.3	392	14	US-10-017-161-808	Sequence 222, App
30	374.5	23.2	387	14	US-10-251-385-222	Sequence 1, Appli
31	374	23.2	319	14	US-10-167-192-1	Sequence 2, Appli
32	374	23.2	319	15	US-10-400-991-4	Sequence 4, Appli
33	372.5	23.1	387	10	US-09-910-334-2	Sequence 2, Appli
34	372.5	23.1	387	15	US-10-619-141-2	Sequence 4, Appli
35	369.5	22.9	339	14	US-10-188-149A-4	Sequence 21, Appli
36	369.5	22.9	387	9	US-09-944-807-21	Sequence 8, Appli
37	369.5	22.9	387	14	US-10-092-135-8	Sequence 108, App
38	369.5	22.9	387	14	US-10-251-385-108	Sequence 4, Appli
39	369.5	22.9	387	14	US-10-240-842-4	Sequence 281, App
40	369.5	22.9	387	14	US-10-225-567A-281	Sequence 4, Appli
41	369.5	22.9	387	14	US-10-296-223-4	Sequence 3, Appli
42	369.5	22.9	387	14	US-10-348-083-3	Sequence 43, Appl
43	369.5	22.9	387	14	US-10-044-643-43	Sequence 224, App
44	369.5	22.9	387	15	US-10-295-027-224	Sequence 224, App
45	369.5	22.9	387	15	US-10-295-027-228	

#### ALIGNMENTS

#### RESULT 1

US-09-768-877-20  
; Sequence 20, Application US/09768877  
; Patent No. US20020150896A1  
; GENERAL INFORMATION:  
; APPLICANT: POLONSKY, KENNETH S.  
; APPLICANT: HORIKAWA, YUKIO  
; APPLICANT: ODA, NAOHISA  
; APPLICANT: COX, NANCY J.  
; APPLICANT: SREENAN, SEAMUS  
; APPLICANT: ZHOU, YUN-PING  
; APPLICANT: OTANI, KENICHI  
; APPLICANT: HANIS, CRAIG L.  
; APPLICANT: BELL, GRAEME I.  
; TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES  
; FILE REFERENCE: ARCD:307  
; CURRENT APPLICATION NUMBER: US/09/768,877  
; CURRENT FILING DATE: 2001-01-23  
; PRIOR APPLICATION NUMBER: 09/422,869  
; PRIOR FILING DATE: 1999-10-21  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Human  
US-09-768-877-20

Query Match 99.6%; Score 1609; DB 9; Length 309;  
Best Local Similarity 99.7%; Pred. No. 5.3e-147;  
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MNGYNTCGSSDLTWPPAIAKLGFGVAYLGLVLLGLLNSLALWVFCRCMQQTETRIYMT 60

Db 1 MNGYNTCGSSDLTWPPAIAKLGFGVAYLGLVLLGLLNSLALWVFCRCMQQTETRIYMT 60

Qy	61	NI	AVADICLLCTLPVLHSLRDTSTPLCQLSQGLYLTNRYSISILVTAIAVDRYVAVRH	120
Db	61	NI	AVADICLLCTLPVLHSLRDTSTPLCQLSQGLYLTNRYSISILVTAIAVDRYVAVRH	120
Qy	121	PL	RAGLRSPQAAVCAVLWLVITGSLVARMLLGIQEGGFCFRSTRHNFNSMRPFLGCF	180
Db	121	PL	RAGLRSPQAAVCAVLWLVITGSLVARMLLGIQEGGFCFRSTRHNFNSMRPFLGCF	180
Qy	181	YL	PLAVVVVFCSLKVVTALAQRPPTDVGQAEATRKAKRMVWANLLVFVVCFLPLHVLGLTVR	240
Db	181	YL	PLAVVVVFCSLKVVTALAQRPPTDVGQAEATRKAKRMVWANLLVFVVCFLPLHVLGLTVR	240
Qy	241	LA	VGNACALLETIRRALYITSKLSDANCLDLAI CYYWAKEFQESALAVAPRAKAHKS	300
Db	241	LA	VGNACALLETIRRALYITSKLSDANCLDLAI CYYWAKEFQESALAVAPRAKAHKS	300
Qy	301	QD	SLCVTLA 309	
Db	301	QD	SLCVTLA 309	

RESULT 2  
 US-10-225-567A-492  
 ; Sequence 492, Application US/10225567A  
 ; Publication No. US20030113798A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LifeSpan Biosciences  
 ; APPLICANT: Brown, Joseph P.  
 ; APPLICANT: Burner, Glenna C.  
 ; APPLICANT: Roush, Christine L.  
 ; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
 ; FILE REFERENCE: 1920-4-4  
 ; CURRENT APPLICATION NUMBER: US/10/225,567A  
 ; CURRENT FILING DATE: 2001-12-19  
 ; PRIOR APPLICATION NUMBER: 60/257,144  
 ; PRIOR FILING DATE: 2000-12-19  
 ; NUMBER OF SEQ ID NOS: 2292  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 492  
 ; LENGTH: 309  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-225-567A-492

Query Match	99.6%;	Score 1609;	DB 14;	Length 309;
Best Local Similarity	99.7%;	Pred. No. 5.3e-14;		
Matches 308;	Conservative 0;	Mismatches- 1;	Indels 0;	Gaps 0;
Qy	1	MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVIGLLNLSLAWVFCRMRQOWTETRIYMT	60	
Db	1	MNGTYNTCGSSDLTWPPAIKLGFYAYLGVLLVIGLLNLSLAWVFCRMRQOWTETRIYMT	60	
Qy	61	NLAVADLCCLCTLPFLVHLSLRDTSPTPLCQLSQGIYLTNRYSISLVTAIADVRYAVRH	120	
Db	61	NLAVADLCCLCTLPFLVHLSLRDTSPTPLCQLSQGIYLTNRYSISLVTAIADVRYAVRH	120	
Qy	121	PLRARGLSRPROAAAVCAVLWLVITGSLVARWLLGIQSGGFCFRSTRNFNSMRPPLLGCF	180	
Db	121	PLRARGLSRPROAAAVCAVLWLVITGSLVARWLLGIQSGGFCFRSTRNFNSMRPPLLGCF	180	
Qy	181	YLPLAVVVFCSLKVYTALAQRPPTDVGQAEATRKARVMWANLLVVFVFCFLPHVGLTVR	240	
Db	181	YLPLAVVVFCSLKVYTALAQRPPTDVGQAEATRKARVMWANLLVVFVFCFLPHVGLTVR	240	
Qy	241	LAVGHNACALLETIRRALYIITSKLSANDCCLDAI CYYVMKEFQBSALAVAPRAKAHKS	300	
Db	241	LAVGHNACALLETIRRALYIITSKLSANDCCLDAI CYYVMKEFQBSALAVAPRAKAHKS	300	
Qy	301	QDSL CVTLA 309		
Db	301	QDSL CVTLA 309		

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RESULT 3
US-10-696-639-44
; Sequence 44, Application US/10696639
; Publication No. US20050037439A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corporation
; APPLICANT: Bourner, Maureen J.
; TITLE OF INVENTION: DIFFERENTIALLY EXPRESSED GENES INVOLVED IN CANCER, THE
; TITLE OF INVENTION: POLYPEPTIDES ENCODED THEREBY, AND METHODS OF USING THE SAME
; FILE REFERENCE: 01040/1
; CURRENT APPLICATION NUMBER: US/10/696,639
; CURRENT FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/422,176
; PRIOR FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 3114
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 309
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-696-639-44

```

```

RESULT 4
US-10-157-031-351
; Sequence 351, Application US/10157031
; Publication No. US2003010890A1
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobashev, A. V.
; APPLICANT: Krukovskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157,031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 351
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-031-351

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Query Match 98.9%; Score 1597; DB 14; Length 309;  
Best Local Similarity 99.0%; Pred. No. 7.6e-146;  
Matches 306; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MNGYNTCGSSDLTPWPAIKLGFYAYLGVLVGLLLNSLALWVFCRMOQWTEIRIYMT 60  
DB 1 MNGYNTCGSSDLTPWPAIKLGFYAYLGVLVGLLLNSLALWVFCRMOQWTEIRIYMT 60

QY 61 NLAVADCLLCTLPVFLHSLRSDTSLCQISQGIYLTNRNYSISLVTAIADRVAVRH 120  
DB 61 NLAVADCLLCTLPVFLHSLRSDTSLCQISQGIYLTNRNYSISLVTAIADRVAVRH 120

QY 121 PLRAGLSRPROAAVCAVLVLTGSLVARWLLGIQSGFCFRSTRNFNSMRPFLG 180  
DB 121 PLRAGLSRPROAAVCAVLVLTGSLVARWLLGIQSGFCFRSTRNFNSMRPFLG 180

QY 181 YPLAVVVFCSLKVVYTAQRPPTDVQAEATRKAKRWANLLVFVVCFLPLHGLTVR 240  
DB 181 YPLAVVVFCSLKVVYTAQRPPTDVQAEATRKAKRWANLLVFVVCFLPLHGLTVR 240

QY 241 LAVGNACALLETIRRALYITSKLSDANCCLDACIYYYMAKEFOEASALAVAPRAKAHKS 300  
DB 241 LAVGNACALLETIRRALYITSKLSDANCCLDACIYYYMAKEFOEASALAVAPRAKAHKS 300

QY 301 QDSLCTVLA 309  
DB 301 QDSLCTVLA 309

## RESULT 5

US-09-964-821B-11  
; Sequence 11, Application US/09964821B  
; Publication No. US20030186360A1  
; GENERAL INFORMATION:  
; APPLICANT: FEDER, J. N.  
; APPLICANT: MINTIER, G.  
; APPLICANT: RAMANATHAN, C. S.  
; APPLICANT: HAWKEN, D.R.  
; APPLICANT: CACACE, A.  
; APPLICANT: BARBER, L.  
; APPLICANT: KORNACKER, M. G.  
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMV3,  
; FILE REFERENCE: D0042NP  
; CURRENT APPLICATION NUMBER: US/09/964,821B  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: 60/235,713  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/261,783  
; PRIOR FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: 60/305,085  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 60/313,171  
; PRIOR FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-964-821B-11

Query Match 24.8%; Score 401; DB 10; Length 370;  
Best Local Similarity 34.1%; Pred. No. 3.2e-30;  
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AYLVGLLVGLLLNSLALWVFCRMOQWTEIRIYMTNLAVADCLLCTLPF-VLHSLR-- 81  
DB 44 AVYSVVFILGLTNSVLSLVFVFCRMRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103

QY 82 -DTSPTPLCQISQGIYLTNRNYSISLVTAIADRVAVRHPLRAGLSRPROAAVCAVL 140  
DB 104 WPFQDT-LCKISGTAFLNIYGSMLFLTCISVDRLAIVYPRSTRIRNRSAIVCAGV 162

QY 141 WVLVIGSLVARWLLGIQE-----GGFCFRSTRHNFNSMR--FPLLGFLPLAVVVF 189  
DB 163 WILVLSGGISASLFTSTNNVNNATTTTCFEGFSKRVKWTYLSKITIFIEVVGFIIPLNVS 222

QY 190 CSLKVVYTAQRPPTDVQAEAT-RKAKRWANLLVFVVCFLPLHGLTVRLAVGNAC 248  
DB 223 CSSVVLRTL--RKPATLSQIGTNKKVKLMITVHMAVFVVCVPYNSVLFVALVRSQAI 280

QY 249 --ALLETIRRALY-ITSKLSDANCCLDACIYYYMAKEFOEASALAVAPRAKAHKSODSLC 305  
DB 281 TNCFLERFAKIMYPITLCLATLNCDFDPIYYFTLESFQKSFYI-----NAHIRMESLF 334

QY 306 VT 307  
DB 335 KT 336

## RESULT 6

US-10-081-810-44  
; Sequence 44, Application US/10081810  
; Publication No. US20030064438A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR NUCLEIC ACIDS, POLYPEPTIDES, ANTIBODI  
; FILE REFERENCE: D0132 NP  
; CURRENT APPLICATION NUMBER: US/10/081,810  
; CURRENT FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: US 60/270,793  
; PRIOR FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: US 60/270,792  
; PRIOR FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: US 60/296,427  
; PRIOR FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 44  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-081-810-44

Query Match 24.8%; Score 401; DB 14; Length 370;  
Best Local Similarity 34.1%; Pred. No. 3.2e-30;  
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AYLVGLLVGLLLNSLALWVFCRMOQWTEIRIYMTNLAVADCLLCTLPF-VLHSLR-- 81  
DB 44 AVYSVVFILGLTNSVLSLVFVFCRMRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103

QY 82 -DTSPTPLCQISQGIYLTNRNYSISLVTAIADRVAVRHPLRAGLSRPROAAVCAVL 140  
DB 104 WPFQDT-LCKISGTAFLNIYGSMLFLTCISVDRLAIVYPRSTRIRNRSAIVCAGV 162

QY 141 WVLVIGSLVARWLLGIQE-----GGFCFRSTRHNFNSMR--FPLLGFLPLAVVVF 189  
DB 163 WILVLSGGISASLFTSTNNVNNATTTTCFEGFSKRVKWTYLSKITIFIEVVGFIIPLNVS 222

QY 190 CSLKVVYTAQRPPTDVQAEAT-RKAKRWANLLVFVVCFLPLHGLTVRLAVGNAC 248  
DB 223 CSSVVLRTL--RKPATLSQIGTNKKVKLMITVHMAVFVVCVPYNSVLFVALVRSQAI 280

QY 249 --ALLETIRRALY-ITSKLSDANCCLDACIYYYMAKEFOEASALAVAPRAKAHKSODSLC 305  
DB 281 TNCFLERFAKIMYPITLCLATLNCDFDPIYYFTLESFQKSFYI-----NAHIRMESLF 334

QY 306 VT 307  
DB 335 KT 336

## RESULT 7

;	PRIOR APPLICATION NUMBER: JP0088912/2001		
;	PRIOR FILING DATE: 2001-03-26		
;	PRIOR APPLICATION NUMBER: JP402288/2000		
;	PRIOR FILING DATE: 2000-12-28		
;	NUMBER OF SEQ ID NOS: 182		
;	SOFTWARE: PatentIn Ver. 2.0		
;	SEQ ID NO 176		
;	LENGTH: 370		
;	TYPE: PRT		
;	ORGANISM: Homo sapiens		
;	US-10-024-298A-176		
	Query Match	24.8%; Score 401; DB 14; Length 370;	
	Best Local Similarity	34.1%; Pred. No. 3.2e-30;	
	Matches 103; Conservative	60; Mismatches 111; Indels 28; Gaps 10;	
QY	25	AYVGLLVGLLNSLAWFCRCMQQWETRIYMTNLAVADLCLLCTLP-VLHSLR-- 81	
DB	44	AVSVVFIIGLITNSVSLFVFCPRKQRSTAIPTNLAVSDLLFVCTLPFKIFNFRH 103	
QY	82	-DTSDDPLCQLSGIYLTNRYMSISLVTALADRYVAVRHLRARGLSPRQAAACAVL 140	
DB	104	WPGGDT-LCKISGTAFLTNYGSMFLFTCLISVDRFLAIVPFSRTTTRNSAIVCAGV 162	
QY	141	WLVIGSLVARWLLGIQE-----GGFCFSTRHFNMSR--FPLLGYPILPAVVVF 189	
DB	163	WILVLSGGISASLFTSTNVNNAATTCTCEGFSKRVKTYLSKITIFIEVGVFIILPLNVS 222	
QY	190	CSLKVVTTALAQRPPTDVQAEAT-RKAKRMVWALLVFPVCFPLHVLTVRLAVGNAC 248	
DB	223	CSWVLRTL--RKPAFLSQIGTNNKKVLYMTVHMAVFPVCFPYNVSLFLYALVRQAI 280	
QY	249	--ALLTIRRALY-ITSKLSDANCCLDAICYYYMAKEFOBASALAVAPRAKAHKSQDSL 305	
DB	281	TNCFLERFAXIMYPITLCIATLNCCTPPFIYFTLESFQSKFYI-----NAHIRMESLF 334	
QY	306	VT 307	
DB	335	KT 336	
	RESULT 9		
	US-10-042-211A-176		
	; Sequence 176, Application US/10042211A		
	; Publication No. US20030170719A1		
	; GENERAL INFORMATION:		
	; APPLICANT: MATSUDA, Akio et al.		
	; TITLE OF INVENTION: NFKB Activating Gene		
	; FILE REFERENCE: 1254-0192P		
	; CURRENT APPLICATION NUMBER: US/10/042,211A		
	; CURRENT FILING DATE: 2002-01-11		
	; PRIOR APPLICATION NUMBER: JP 2000-402288		
	; PRIOR FILING DATE: 2000-12-28		
	; PRIOR APPLICATION NUMBER: JP 2001-088912		
	; PRIOR FILING DATE: 2001-03-26		
	; PRIOR APPLICATION NUMBER: JP 2001-254018		
	; PRIOR FILING DATE: 2001-08-24		
	; PRIOR APPLICATION NUMBER: US 60/258,315		
	; PRIOR FILING DATE: 2000-12-28		
	; PRIOR APPLICATION NUMBER: US 60/278,640		
	; PRIOR FILING DATE: 2001-03-26		
	; PRIOR APPLICATION NUMBER: US 60/314,385		
	; PRIOR FILING DATE: 2001-08-24		
	; NUMBER OF SEQ ID NOS: 182		
	; SOFTWARE: PatentIn Ver. 2.0		
	; SEQ ID NO 176		
	; LENGTH: 370		
	; TYPE: PRT		
	; ORGANISM: Homo sapiens		
	; US-10-042-211A-176		
	Query Match	24.8%; Score 401; DB 14; Length 370;	
	Best Local Similarity	34.1%; Pred. No. 3.2e-30;	



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; Sequence 86, Application US/10753267
; Publication No. US20050037946A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Stagliano, Nancy E.
; APPLICANT: Healy, Aileen
; APPLICANT: Acton, Susan L.
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Donoghue, Mary A.
; APPLICANT: Rodriguez-Way, Amelie
; APPLICANT: Tomlinson, James E.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1722, 10280, 59917, 85553,
; TITLE OF INVENTION: 10653, 9235, 21668, 17794, 2210, 6169, 10102, 21061, 17662,
; TITLE OF INVENTION: 1468, 12282, 6350, 9035, 1820, 23652, 7301, 8925, 8701,
; TITLE OF INVENTION: 3533, 9462, 9133, 12788, 17729, 65552, 1261, 21476, 33770,
; TITLE OF INVENTION: 9380, 2569654, 33556, 44143, 32612, 10671, 261,
; TITLE OF INVENTION: 44570, 41922, 2552, 2417, 19319, 43969, 8921, 8993, 955,
; TITLE OF INVENTION: 32345, 966, 1920, 17318, 1510, 14180, 26005, 554, 16408,
; TITLE OF INVENTION: 42028, 112091, 13886, 13942, 1673, 54946 OR 2419
; FILE REFERENCE: MPI03-003PILNOMTIN
; CURRENT APPLICATION NUMBER: US/10753,267
; CURRENT FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: US 60/439,683
; PRIOR FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/445,216
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/448,036
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/454,189
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/457,541
; PRIOR FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: US 60/466,411
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US 60/469,041
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/477,414
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: US 60/478,560
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/489,772
; PRIOR FILING DATE: 2003-07-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-753-267-86

Query Match 24.8%; Score 401; DB 17; Length 370;
Best Local Similarity 34.1%; Pred. No. 3.2e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AYLGVLVLGLLNSLALWVFCRMOQWTEIYMTNLAVADCLLCTLPF-VLHSLR-- 81
DB 44 AVYSVVFILGLITNSVSLFVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103
QY 82 -DTSPTPLCOLSQGIYLTNRYSISLVTAIADRVYAVRHPLRARGLSRPROQAAVAVL 140
DB 104 WFGDPT-LCKISGTAFLNIYGSMLFLTCISVDRLAIYVPPRSRTIRTRNSAIVCAGV 162
QY 141 WVLVIGSLVARMLLGIQEGE-----GGFCFRSTRHFNFSMR--FPLLGFLVPLAVVVF 189
DB 163 WILVLSGGISASLFSITTNVNNATTTCEGFSKRVKWTYLSKITIFIEVVGFIIPLNVS 222
QY 190 CSLKVVTAALQRPPTDVQAEAT-RKAKRMVWVANLLVFWVCLPLHVLGTVRLAVGWNAC 248
DB 223 CSSVWLRTL--RKPATLSQIGTNKKVKLMITVHMAVFWVCFVFPYNSVLFVALVRSQAI 280
QY 249 --ALLETIRRALY-ITSKLSANDCCLDACIYYMYMAKEFOEASALAVAPRAKAHKSQDSL 305

; Sequence 86, Application US/09964821B
; Publication No. US20030186360A1
; GENERAL INFORMATION:
; APPLICANT: FEDER, J. N.
; APPLICANT: MINTIER, G.
; APPLICANT: RAMANATHAN, C. S.
; APPLICANT: HAWKEN, D.R.
; APPLICANT: CACACE, A.
; APPLICANT: BARBER, L.
; APPLICANT: KORNACKER, M. G.
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRM3,
; TITLE OF INVENTION: EXPRESSED HIGHLY IN IMMUNE- AND COLON- RELATED TISSUES
; FILE REFERENCE: D0042NP
; CURRENT APPLICATION NUMBER: US/09/964,821B
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/235,713
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/261,783
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/305,085
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/313,171
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 370
; TYPE: PRT
; ORGANISM: HUMAN
US-09-964-821B-10

Query Match 24.8%; Score 400; DB 10; Length 370;
Best Local Similarity 34.0%; Pred. No. 4e-30;
Matches 105; Conservative 58; Mismatches 104; Indels 42; Gaps 11;

QY 25 AYLGVLVLGLLNSLALWVFCRMOQWTEIYMTNLAVADCLLCTLPF-VLHSLR-- 81
DB 44 AVYSVVFILGLITNSVSLFVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNFRH 103
QY 82 -DTSPTPLCOLSQGIYLTNRYSISLVTAIADRVYAVRHPLRARGLSRPROQAAVAVL 140
DB 104 WFGDPT-LCKISGTAFLNIYGSMLFLTCISVDRLAIYVPPRSRTIRTRNSAIVCAGV 162
QY 141 WVLVIGSLVARMLLGIQEGE-----CFR-----STRHFNFSMRPPLLGFLY 182
DB 163 WILVLSG-----GISASLFSITTNVNNATTTCEGFSKRVKWTYLSKITIFIEVVGFII 215
QY 183 PLAVVVFCSLKVVTAALQRPPTDVQAEAT-RKAKRMVWVANLLVFWVCLPLHVLGTVRL 241
DB 216 PULNVSCSVVLRTL--RKPATLSQIGTNKKVKLMITVHMAVFWVCFVFPYNSVLFVLA 273
QY 242 AVGNWAC--ALLETIRRALY-ITSKLSANDCCLDACIYYMYMAKEFOEASALAVAPRAKAH 298
DB 274 LVRSQAITNCFLERPAKIMYPITCLATLNCCDFPIYYFTLESFQKSFYI-----NAH 327
QY 299 KSQDSLVCVT 307
DB 328 IRMESLEKT 336

RESULT 14
US-10-268-332-10
; Sequence 10, Application US/10268332
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; Publication No. US20030175748A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRTMY3, EXPRESSED HIGHLY
; TITLE OF INVENTION: IMMUNE- AND COLON- RELATED TISSUES
; FILE REFERENCE: D0042A CIP
; CURRENT APPLICATION NUMBER: US/10/268,332
; PRIORITY FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: U.S. 60/235,713
; PRIORITY FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: U.S. 60/261,783
; PRIORITY FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: U.S. 60/305,085
; PRIORITY FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: U.S. 60/313,171
; PRIORITY FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: U.S. 09/964,821
; PRIORITY FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 10
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-268-332-10

Query Match      24.8%; Score 400; DB 14; Length 370;
Best Local Similarity 34.0%; Pred. No. 4e-30;
Matches 105; Conservative 58; Mismatches 104; Indels 42; Gaps 11;

QY      25  AYLGVLLVGLLLNSLALWFCRMOQWETRIYMTNLAVADCLLCTLPV-VLHSLR-- 81
DB      44  AVYSVVFILGLITNSVSLVFCFRMKRSETAIFITNLAVSLLFVCTLPFKIFYNFRH 103
QY      82  -DTSPTPLCOLSQGIYLTNRVMSISLVTAIAVDVAVVHPLRAGLSRPROAAAACAVL 140
DB      104  WPFQGT-LCKISGTAFLNIYGSMLFLCISVDRFLAIVYPPRSRTIIRNRSAIVCAGV 162
QY      141  WVLVIGSLVARWLLGIQEGF-----CFR-----STRHNFNSMRFPPLGPLYL 182
DB      163  WILVLSG-----GISASLFTTNVNNATTCFEGLSKRVWKTLYLSKITIFIEVVGFI 215
QY      183  PLAVVFCSLKVVTALAORPPDVQAEAT-RKAKRMVWANLLVVFVCFPLHVLGLTVRL 241
DB      216  PLILNVSCSVVRLTL--RKPATLSQIGTNKKVLMITVHMAVFCVFPVNSVLFYA 273
QY      242  AVGNWAC--ALLETIRRALY-ITSKLSDANCCLDAICYYMAKEFOEASALAVAPRAK 298
DB      274  LVRSQAITNCFLERFKIMYPITLCLATLNCDFPFIFYFTLESFQKGYI-----NAH 327
QY      299  KSQDSLQVLT 307
DB      328  IRMESLFKT 336

RESULT 15
US-10-024-298A-174
; Sequence 174, Application US/10024298A
; Publication No. US20030143540A1
; GENERAL INFORMATION:
; APPLICANT: ASAHI KASEI KABUSHIKI KAISHA
; APPLICANT: AKIO MATSUDA
; APPLICANT: Goichi HONDA
; APPLICANT: Shuji MURAMATSU
; APPLICANT: Yukiko NAGANO
; TITLE OF INVENTION: NF-K B Activating Gene
; FILE REFERENCE: 1254-0191P
; CURRENT APPLICATION NUMBER: US/10/024,298A
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/314,385
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/278,641
; PRIOR FILING DATE: 2001-03-26
```

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; PRIOR APPLICATION NUMBER: 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP254018/2001
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: JP0088912/2001
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP402288/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 174
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-298A-174

Query Match      24.2%; Score 391; DB 14; Length 370;
Best Local Similarity 34.5%; Pred. No. 2.9e-29;
Matches 97; Conservative 58; Mismatches 104; Indels 22; Gaps 9;

QY      25  AYLGVLLVGLLLNSLALWFCRMOQWETRIYMTNLAVADCLLCTLPV-VLHSLR-- 81
DB      44  AVYSVVFILGLITNSASLWFCFRMKRSETATFITNLALSLLFVCTLPFKIFYNFRH 103
QY      82  -DTSPTPLCOLSQGIYLTNRVMSISLVTAIAVDVAVVHPLRAGLSRPROAAAACAVL 140
DB      104  WPFQGT-LCKISGTAFLNIYGSMLFLCISVDRFLAIVYPPRSRTIIRNRSAIVCAGV 162
QY      141  WVLVIGSLVARWLLGIQIE-----GGFCFRSTRHNFNSMR--FPLLGFYLPVAVVVF 189
DB      163  WILVLSGGISASLFTTNVNNATTCFEGFSKRVWKTLYLSKITIFIEVVGFIPLILNV 222
QY      190  CSLKVVVTALAORPPDVQAEAT-RKAKRMVWANLLVVFVCFPLHVLGLTVRLAVGNWAC 248
DB      223  CSSVVLRTL--RKPATLSQIGTNKKVLMITVHMAVFCVFPVNSVLFYALVRSQAI 280
QY      249  --ALLETIRRALY-ITSKLSDANCCLDAICYYMAKEFOEA 286
DB      281  TNCLLERFAKIMYPITLCLATLNCDFPFIFYFTLESFQKS 321

Search completed: May 23, 2005, 11:33:03
Job time : 56 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 23, 2005, 11:15:00 ; Search time 17 Seconds  
(without alignments)  
1748.881 Million cell updates/sec

Title: US-10-083-168-85  
Perfect score: 1615  
Sequence: 1 MNGTYNTCGSSDLTPPAIK.....AVAPRAHKQSLSLCTVLA 309

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	400	24.8	370	JC5549	heptahelical P2Y5-
2	369.5	22.9	387	I69202	G protein-coupled
3	367.5	22.8	308	I50241	G protein-coupled
4	359.5	22.3	344	T09508	intron 17 purinerg
5	317	19.6	373	A47556	ATP receptor P2u -
6	316	19.6	362	S33733	G protein-coupled
7	315.5	19.5	365	S68679	G protein-coupled
8	314	19.4	328	I5450	G protein-coupled
9	311.5	19.3	354	I53033	G protein-coupled
10	311.5	19.3	362	A37641	G protein-coupled
11	311.5	19.3	364	J01488	bradykinin B2 rece
12	311.5	19.3	366	O0RTB2	bradykinin recepto
13	309	19.1	342	S13638	platelet-activatin
14	308.5	19.1	362	B57641	G protein-coupled
15	307.5	19.0	362	S68207	G protein-coupled
16	306.5	19.0	375	A34946	P-2U nucleotide re
17	303	18.8	342	A40191	platelet-activatin
18	303	18.8	352	S60024	angiotensin II rec
19	300.5	18.6	373	J04162	chemokine (C-C) re
20	296.5	18.4	373	J04737	P2Y receptor - bov
21	292	18.1	341	S43252	G protein-coupled
22	288	17.8	363	J02543	platelet-activatin
23	286.5	17.7	352	A43113	angiotensin II rec
24	286	17.7	328	J04800	p2Y6 receptor - hu
25	284.5	17.6	361	B45680	G protein-coupled
26	282	17.5	341	S63666	platelet-activatin
27	280.5	17.4	366	I49519	bradykinin B2 rece
28	279.5	17.3	361	J05653	G protein-coupled
29	278.5	17.2	363	I57955	somatostatin recep

30	278.5	17.2	364	2	JN0763	somatostatin recep
31	277	17.2	363	2	A49052	angiotensin II rec
32	274	17.0	363	2	I48261	angiotensin II rec
33	274	17.0	363	2	I57940	somatostatin recep
34	272.5	16.9	365	2	S68208	G protein-coupled
35	270.5	16.7	355	2	I49339	macrophage inflam
36	270.5	16.7	420	2	I51667	thrombin receptor
37	269	16.7	354	2	T09353	G protein-coupled
38	267	16.5	323	1	Q0BED3	HHRF3 protein - hu
39	267	16.5	418	2	A46226	somatostatin recep
40	264.5	16.4	355	2	J05067	G protein-coupled
41	261.5	16.2	359	2	J02134	angiotensin II rec
42	261.5	16.2	369	2	J05068	G protein-coupled
43	261.5	16.2	391	2	A41795	somatostatin recep
44	261.5	16.2	391	2	C41795	somatostatin recep
45	261.5	16.2	391	2	A39297	somatostatin recep

ALIGNMENTS

RESULT 1

JC5549  
heptahelical P2Y5-like receptor - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Sep-1997 #sequence\_revision 05-Sep-1997 #text\_change 09-Jul-2004  
C:Accession: JC5549  
R:Janssens, R.; Boeynaems, J.M.; Godart, M.; Communi, D.  
Biochem. Biophys. Res. Commun. 236, 106-112, 1997  
A:Title: Cloning of a human heptahelical receptor closely related to the P2Y5 receptor.  
A:Reference number: JC5549; MUID:97366605; PMID:9223435  
A:Accession: JC5549  
A:Molecule type: DNA  
A:Residues: 1-370 <JAN>  
C:Cross-references: UNIPROT:Q99677; DBJ:AF005419; NID:g2240034; PIDN:AAB66322.1; PID:g2  
C:Superfamily: ATP receptor P2u

Query Match 24.8%; Score 400; DB 2; Length 370;  
Best Local Similarity 34.0%; Pred. No. 1.8e-29;  
Matches 105; Conservative 58; Mismatches 104; Indels 42; Gaps 11;

Qy	25	AYLGVLVGLGLNLSLALWFCBMOQWETRIYMTNLAVADLCCLCTLPF-VLHSLR--	81
Db	44	AVYSVVFILGUITSVSLVFCFRMKRSETAIFITNLAVSDLLFCVCTLPKIFINRHH	103
Qy	82	-DTSPTPLCOLSQGIYLTNRYSISLVTAIAVDYVAVRHPLRGLRSPQAAAVCAVL	140
Db	104	WPFQGT-LCKISGTAFLTNIGSMLFTCISVDRLAIVYFRSRTITRNSAIVCAGV	162
Qy	141	WLVIGSLVARWLLGIOEGGF-----CFR-----STRHFNNSMRFPPLLGPLY	182
Db	163	WILVLSG-----GISASLFTTNVNNATTCEGLSKRVWKTYLSKITIFIEVVGPII	215
Qy	183	PLAVVFCSLKVVTAQRPETDVGQAEAT-RKAKRWVWVWNLVYVVCFLPLHVLGTVRL	241
Db	216	PLILNVSCSVVLRTL--RKPTATLSQIGTNKKKVLKMTVMHMAVFWVFCVYNSVLFYLA	273
Qy	242	AVGNWAC--ALLETIRALY-ITSKLSDANCLDAICYVMYMAKEFOEASALAVAPRAKAH	298
Db	274	LVRQAITNCFLEFAKIMYFITCLATLNCDFPIFYFTLESFQKSFYI-----NAH	327
Qy	299	KSQDSLQVLT 307	
Db	328	IRMESLFKT 336	

RESULT 2

I69202  
G protein-coupled receptor HM74 - human  
C:Species: Homo sapiens (man)  
C:Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 09-Jul-2004  
C:Accession: I69202  
R:Nomura, H.; Nielsen, B.W.; Matsushima, K.





Db 294 TSDITIONS 301

RESULT 5

A47556

ATP receptor P2u - mouse

C:Species: Mus musculus (house mouse)

C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004

C:Accession: A47556

R:Jushtig, K.D.; Shlau, A.K.; Brake, A.J.; Julius, D.

Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993

A:Title: Expression cloning of an ATP receptor from mouse neuroblastoma cells.

A:Reference number: A47556; MUID:93281707; PMID:7685114

A:Accession: A47556

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-373 <LUS>

A:Cross-references: UNIPROT:P35383; GB:L14751; NID:G309457; PIDN:AAA39871.1; PID:G309458

C:Superfamily: ATP receptor P2u

C:Keywords: transmembrane protein

Query Match 19.6%; Score 317; DB 2; Length 373;

Best Local Similarity 30.1%; Pred. No. 9.2e-22;

Matches 101; Conservative 54; Mismatches 130; Indels 50; Gaps 11;

QY 2 NGTYNCGSSDLTWPAPKLG- - - - -YAYL- - - - -GVLLVLGLLNSLALWVFCR 48

Db 9 NSTINGWEGD- - - - -ELGKCRFNEDEKVLPLPVSYGVVGVVGLCLNVVALVFLCR 61

QY 49 MQQWTEIRYMTNLAVADCLCTLPFLVHSLRDTSDTP- - - - -LCQLSQGYLTVRYMSI 104

Db 62 LKTNWASTYMPHLAVSDLSYAAASLPLVYVYARGDHPFSTVLCVLRFLFYTNLYCSI 121

QY 105 SLVTAIAVDYVAVRHPLRARGLRSPROAAACAVLWLVIGSLVARWLLGQEGGFCPR 164

Db 122 LFTLCISVHRCLGVLRPLHSLRWGRYARVAAVWVLLV-ACQAPVLYFTTSGRTR 180

QY 165 STRHN- - - - -FNSMRFPLLGFLPLVAVVFCSLKVVVTAQAQPP- - - - -TDVGQAE 210

Db 181 ITCHDTSARELPSHFVSSVMGLL-FAVPFSVLVCVLMARLL-KPAYGTTGGLPR 238

QY 211 ATRKAKRMWVANLLVFFVVCFLPLHVLGTVRLAVGH- - - - -NACALLETIRRALYITSKLSDAN 268

Db 239 AKRKSVRTIALVAVFALCFPLFHTVTRTYYSFRSLDSCHTLNINWAYKITRPLASAN 298

QY 269 CCLDAICVYY- - - - -MAKEQAEASALAVAPRAK 296

Db 299 SCLDPVLYFLAGQLRVRFARDAKPTEPTSPQAR 333

RESULT 6

S33733

G protein-coupled receptor - chicken

C:Species: Gallus gallus (chicken)

C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004

C:Accession: S33733

R:Webb, T.E.; Simon, J.; Krishnek, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.; Burnstock

FEBS Lett. 324, 219-225, 1993

A:Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor.

A:Reference number: S33733; MUID:93285340; PMID:8508924

A:Accession: S33733

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-362 <WEB>

A:Cross-references: UNIPROT:P34996; EMBL:X73268; NID:G395084; PIDN:CAA51716.1; PID:G39509

C:Superfamily: ATP receptor P2u

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 19.6%; Score 316; DB 2; Length 362;

Best Local Similarity 28.2%; Pred. No. 1.1e-21;

Matches 96; Conservative 63; Mismatches 134; Indels 48; Gaps 12;

QY 2 NGTYNCGSSDLTWPAPKLG- - - - -YAYL- - - - -GVLLVLGLLNSLALWVFCR 48

Db 9 NSTINGWEGD- - - - -ELGKCRFNEDEKVLPLPVSYGVVGVVGLCLNVVALVFLCR 61

QY 49 MQQWTEIRYMTNLAVADCLCTLPFLVHSLRDTSDTP- - - - -LCQLSQGYLTVRYMSI 104

Db 62 LKTNWASTYMPHLAVSDLSYAAASLPLVYVYARGDHPFSTVLCVLRFLFYTNLYCSI 121

QY 105 SLVTAIAVDYVAVRHPLRARGLRSPROAAACAVLWLVIGSLVARWLLGQEGGFCPR 164

Db 122 LFTLCISVHRCLGVLRPLHSLRWGRYARVAAVWVLLV-ACQAPVLYFTTSGRTR 180

QY 165 STRHN- - - - -FNSMRFPLLGFLPLVAVVFCSLKVVVTAQAQPP- - - - -TDVGQAE 210

Db 181 ITCHDTSARELPSHFVSSVMGLL-FAVPFSVLVCVLMARLL-KPAYGTTGGLPR 238

QY 211 ATRKAKRMWVANLLVFFVVCFLPLHVLGTVRLAVGH- - - - -NACALLETIRRALYITSKLSDAN 268

Db 239 AKRKSVRTIALVAVFALCFPLFHTVTRTYYSFRSLDSCHTLNINWAYKITRPLASAN 298

QY 269 CCLDAICVYY- - - - -MAKEQAEASALAVAPRAK 296

Db 299 SCLDPVLYFLAGQLRVRFARDAKPTEPTSPQAR 333

RESULT 7

S68679

G protein-coupled receptor - human

C:Species: Homo sapiens (man)

C>Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004

C:Accession: S68679

R:Stam, N.J.; Klomp, J.; van de Heuvel, M.; Olijve, W.

FEBS Lett. 384, 260-264, 1996

A:Title: Molecular cloning and characterization of a novel orphan receptor (P(2P)) expr:

A:Reference number: S68679; MUID:96197801; PMID:8617367

A:Accession: S68679

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-365 <STA>

A:Cross-references: UNIPROT:P51582; EMBL:X96597; NID:G1296631; PIDN:CAA65415.1; PID:G1296631

C:Superfamily: ATP receptor P2u

C:Keywords: G protein-coupled receptor

Query Match 19.5%; Score 315.5; DB 2; Length 365;

Best Local Similarity 29.2%; Pred. No. 1.2e-21;

Matches 94; Conservative 56; Mismatches 123; Indels 49; Gaps 12;

QY 29 VLLVLGLLNSLALWVFCRMOQWTEIRYMTNLAVADCLCTLPFLVHSLRDTSDTP- 87

Db 44 VVFLGLGLNAPTLLWLFIRLRPMDATATYMPHLASDLYVLSLPTLIYYAAHNHWP 103

QY 88 - - - - -LCQLSQGYLTVRYMSISLVTAIAVDYVAVRHPLRARGLRSPROAAACAVLWLV 144

Db 104 GTEICKFVRFLFYNNLYCSVFLTCISVHRYLGICHPRLARLWGRPRLAGLCLAVLV 163

QY 145 IGSILVAR-WLIGIQEGG- - - - -FCFRSTR- - - - -H- - - - -FNSMRFPLLGFLPLVAVVFCSLK 193

Db 164 AGCLVPNLPFFVTTNKGTTVLCHDTRPEEPDHYVHFSSAVNGLL-FGVPCLVTVCYGL 222

QY 194 VVTAQAQPPTDVGQAEATRAK- - - - -RMVWVANLLVFFVVCFLPLHVLGTV- - - - -RLAVGWNA 247

Db 223 MARRLYQPLP- - - - -GSAQSSRLRSURTAVLVITFAVCFVPPHITRTIYLARLLEA- - - - -D 277

QY 248 CALLETIRRALYITSKLSDANCCCLDAICVYVMAKEFOE- - - - -ASALAV 291

Db 278 CRVLNIVNVVYKTRPLASNSCLDPVLYLLTGDKYRRLQLCGGKPPQPTAASSLAL 337

QY 292 APRAK- - - - -AHKSQDSLCVT 307

Db 338 VSLPEDSSCRWAATPDSSCST 359

RESULT 8

QY 1 MNGTY- - - - -NTCGSSDLTWPAPKLG- - - - -YAYLGVLLVL- - - - -GILLNSLALWV 44

Db 10 LMGTOPELLAGGAAAGNATTKCSLT- - - - -KTGFQFYLLPTVYILVFFITGFLGNSVAIWM 64

QY 45 FCCRMQOWTEIRYMTNLAVADCLCTLPFLVHSLRDTSD- - - - -TPLCOLSGOGLYLTNR 100

Db 65 FVFHMRPWSGISVYMFNLADFLVLTLPALIFYFYFNKTDWIFGDVMCKLQRFIFHVL 124

QY 101 YMSISLVTAIAVDYVAVRHPLRARGLRSPROAAACAVLWLVIGSLVARWLL- - - - -GI 156

Db 125 YGSILFLTCISVHRYTGVVHPLKSLGRLLKKNQAVTVSSLVWALV- - - - -AVIAPILFYSGTG 183

QY 157 QEGG- - - - -FCFRSTRNF- - - - -NSMRFPLLGFLPLVAVVFCSLKVVVTAQAQPPTDVQ 208

Db 184 RNNKITCYDITDADEYLSRYFVYSMCTTVMFCIPFIVILGICYGLIVKALYK- - - - -DLON 240

QY 209 AEATRKAKRMWVANLLVFFVVCFLPLHVLGTVRLAVGWN- - - - -ACALLETIRRALYITSK 263

Db 241 SPLRKSIVLVIIVLTVFAVSVLPFHVMTLNRLARLDFQTPQMCAFNQKVATYQVTRG 300

QY 264 LSDANCCCLDAICVYVMAKEFOEASALAVAPRAKHKSQDSL 304

Db 301 LASLNSCVDPILYFLAGDTFRR- - - - -RLSRATRKSSRRSEPNV 339

RESULT 7

S68679

G protein-coupled receptor - human

C:Species: Homo sapiens (man)

C>Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004

C:Accession: S68679

R:Stam, N.J.; Klomp, J.; van de Heuvel, M.; Olijve, W.

FEBS Lett. 384, 260-264, 1996

A:Title: Molecular cloning and characterization of a novel orphan receptor (P(2P)) expr:

A:Reference number: S68679; MUID:96197801; PMID:8617367

A:Accession: S68679

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-365 <STA>

A:Cross-references: UNIPROT:P51582; EMBL:X96597; NID:G1296631; PIDN:CAA65415.1; PID:G1296631

C:Superfamily: ATP receptor P2u

C:Keywords: G protein-coupled receptor

Query Match 19.5%; Score 315.5; DB 2; Length 365;

Best Local Similarity 29.2%; Pred. No. 1.2e-21;

Matches 94; Conservative 56; Mismatches 123; Indels 49; Gaps 12;

QY 29 VLLVLGLLNSLALWVFCRMOQWTEIRYMTNLAVADCLCTLPFLVHSLRDTSDTP- 87

Db 44 VVFLGLGLNAPTLLWLFIRLRPMDATATYMPHLASDLYVLSLPTLIYYAAHNHWP 103

QY 88 - - - - -LCQLSQGYLTVRYMSISLVTAIAVDYVAVRHPLRARGLRSPROAAACAVLWLV 144

Db 104 GTEICKFVRFLFYNNLYCSVFLTCISVHRYLGICHPRLARLWGRPRLAGLCLAVLV 163

QY 145 IGSILVAR-WLIGIQEGG- - - - -FCFRSTR- - - - -H- - - - -FNSMRFPLLGFLPLVAVVFCSLK 193

Db 164 AGCLVPNLPFFVTTNKGTTVLCHDTRPEEPDHYVHFSSAVNGLL-FGVPCLVTVCYGL 222

QY 194 VVTAQAQPPTDVGQAEATRAK- - - - -RMVWVANLLVFFVVCFLPLHVLGTV- - - - -RLAVGWNA 247

Db 223 MARRLYQPLP- - - - -GSAQSSRLRSURTAVLVITFAVCFVPPHITRTIYLARLLEA- - - - -D 277

QY 248 CALLETIRRALYITSKLSDANCCCLDAICVYVMAKEFOE- - - - -ASALAV 291

Db 278 CRVLNIVNVVYKTRPLASNSCLDPVLYLLTGDKYRRLQLCGGKPPQPTAASSLAL 337

QY 292 APRAK- - - - -AHKSQDSLCVT 307

Db 338 VSLPEDSSCRWAATPDSSCST 359

RESULT 8



A:Reference number: JH0712; MUID:93038601; PMID:1329734  
A:Accession: JH0712  
A:Molecule type: DNA  
A:Residues: 1-364 <EGG>  
A:Cross-references: UNIPROT:P30411; GB:S45489; NID:g256536; PIDN:AAB23467.1; PID:g256537  
R:Powell, S.J.; Slyn, G.; Thomas, C.; Hopkins, B.; Briggs, I.; Graham, A.  
Genomics 15, 435-438, 1993  
A:Title: Human bradykinin B2 receptor: nucleotide sequence analysis and assignment to chromosome 15  
A:Reference number: A46022; MUID:93194199; PMID:7916737  
A:Accession: A46022  
A:Molecule type: DNA  
A:Status: preliminary  
A:Residues: 1-364 <POW>  
A:Cross-references: GB:S56772; NID:g298604; PIDN:AAB25765.1; PID:g298605  
A:Note: sequence extracted from NCBI Backbone (NCBIN:127280, NCBI:P:127284)  
R:Ma, J.; Wang, D.; Ward, D.C.; Chen, L.; Dessai, T.; Chao, J.; Chao, L.  
Genomics 23, 362-369, 1994  
A:Title: Structure and chromosomal localization of the gene (BDKRB2) encoding human bradykinin B2 receptor  
A:Reference number: A55559; MUID:95137582; PMID:7835885  
A:Accession: A55559  
A:Molecule type: DNA  
A:Residues: 1-364 <MAA>  
A:Cross-references: GB:L27594  
R:Hess, J.F.; Borkowski, J.A.; Young, G.S.; Strader, C.D.; Ransom, R.W.  
Biochem. Biophys. Res. Commun. 184, 260-268, 1992  
A:Title: Cloning and pharmacological characterization of a human bradykinin (BK-2) receptor  
A:Reference number: JQ1488; MUID:92231936; PMID:1314587  
A:Accession: JQ1488  
A:Molecule type: mRNA  
A:Residues: 1-364 <HES>  
A:Cross-references: GB:M88714; NID:g1387999; PIDN:AAB02793.1; PID:g1388000  
C:Genetics:  
A:Gene: GDB:BDKRB2  
A:Cross-references: GDB:L35713; OMIM:113503  
A:Map position: 14q32.1-14q32.2  
A:Map: #status absent  
A:Introns: #status absent  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein  
F:34-56/Domain: transmembrane #status predicted <TM1>  
F:66-92/Domain: transmembrane #status predicted <TM2>  
F:104-127/Domain: transmembrane #status predicted <TM3>  
F:148-171/Domain: transmembrane #status predicted <TM4>  
F:195-221/Domain: transmembrane #status predicted <TM5>  
F:241-266/Domain: transmembrane #status predicted <TM6>  
F:285-309/Domain: transmembrane #status predicted <TM7>  
F:312-180/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:170,237,342/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted  
F:242/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted  
F:316/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 19.3%; Score 311.5; DB 2; Length 364;  
Best Local Similarity 27.6%; Pred. No. 2.9e-21;  
Matches 89; Conservative 54; Mismatches 128; Indels 51; Gaps 9;

Qy 1 MNGTYNTCGSSDLTW-----PPAIKLGFYAYLGLVLLGLLNSLALVVFCCRMQOW 52  
Db 11 LNGTFAQSKCQVWGLWLTQPP-----FLWLVFLVLTLENIFVLSVFCFLKSSC 62

Qy 53 TETRIYMTNLAVADICLLCTLPVLSLRLTSD-----TPICQLSQGIYLTNRYMSISLVT 108  
Db 63 TVAEIYLGNTLAADLILACGLFPFWAITISNFDLFGSETLCRVNNAISMNLYSSICFLM 122

Qy 109 AIAVDYVAVRHLRARGLRSPQAAVCAVLW--VLVIGS--LVARWLLGIOGGGFCFR 164  
Db 123 LVSIDRYALVKTMSGMGRGVRAKLYSLVINGCTLLSSPMLVFRMTKYSDEG----- 178

Qy 165 STRHN-----FNSMRFPFLGFLYFLAVVFCSLKVVTALAQRPPTDVGQA 209  
Db 179 --HNVTAQVTSPLSIWVFTNMLNVVGLPLSVITFTCTMQIMQVLRNNEKQKFEI 235

Qy 210 EATKAKRMWVWNLVVFVVCFLPHVGLTV-----RLAVGNACALLETTIRRALYITSKLS 265  
Db 236 QTERATVLLVLLFLICWLPQISTFLDTHRLGLI--LSSCQDERIIDVITQIASPMA 294

Qy 266 DANCCLDAICYNNAKSFQEQAS 287  
Db 295 YSNSCLNPLVYVVGKFRPKS 316

## RESULT 12

## CORTB2

bradykinin receptor type B-2 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text\_change 09-Jul-2004

C:Accession: A41283; A55079; S47529

R:McEachern, A.E.; Shelton, E.R.; Bhakta, S.; Oberholte, R.; Bach, C.; Zuppan, P.; Fujis

Proc. Natl. Acad. Sci. U.S.A. 88, 7724-7728, 1991

A:Title: Expression cloning of a rat B-2 bradykinin receptor.

A:Reference number: A41283; MUID:91352062; PMID:1715575

A:Accession: A41283

A:Molecule type: mRNA

A:Residues: 1-366 <MCE>

A:Cross-references: UNIPROT:P25023; GB:M59967

R:Pesquero, J.B.; Lindsey, C.J.; Zeh, K.; Paiva, A.C.M.; Ganten, D.; Bader, M.

J. Biol. Chem. 269, 26920-26925, 1994

A:Title: Molecular structure and expression of rat bradykinin B2 receptor gene. Evidence

A:Reference number: A55079; MUID:95014558; PMID:7929432

A:Accession: A55079

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-75,'A',77-366 <PES>

A:Cross-references: GB:X80187; GB:X80188; GB:X80189; GB:X80190

R:Wang, D.; Ma, J.; Chao, L.; Chao, J.

Biochim. Biophys. Acta 1219, 171-174, 1994

A:Title: Molecular cloning and sequence analysis of rat bradykinin B(2) receptor gene.

A:Reference number: S47529; MUID:94368850; PMID:8086459

A:Accession: S47529

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-366 <WAN>

A:Cross-references: EMBL:L26173; NID:g476749; PIDN:AAAC2492.1; PID:g685244

C:Comment: This G protein-coupled receptor binds the nonapeptide bradykinin.

C:Superfamily: vertebrate rhodopsin

C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; lipoprotein;

F:31-48/Domain: transmembrane #status predicted <TM1>

F:79-96/Domain: transmembrane #status predicted <TM2>

F:107-126/Domain: transmembrane #status predicted <TM3>

F:154-170/Domain: transmembrane #status predicted <TM4>

F:197-215/Domain: transmembrane #status predicted <TM5>

F:245-261/Domain: transmembrane #status predicted <TM6>

F:314,182/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:105-186/Disulfide bonds: #status predicted

F:326/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 19.3%; Score 311.5; DB 1; Length 366;

Best Local Similarity 28.1%; Pred. No. 2.9e-21;

Matches 90; Conservative 54; Mismatches 127; Indels 49; Gaps 9;



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 23, 2005, 11:07:54 ; Search time 63 Seconds  
(without alignments)  
1896.968 Million cell updates/sec

Title: US-10-083-168-85  
Perfect score: 1615  
Sequence: 1 MNGYNTCGSSDLTWPPAIK.....AVAPRAKHSQDSLCTVLA 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Geneseq1980s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001s:\*
- 5: Geneseq2002s:\*
- 6: Geneseq2003as:\*
- 7: Geneseq2003bs:\*
- 8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1615	100.0	309	5	ABG95172 Human GPC
2	1609	99.6	309	3	AAY79576 Human G p
3	1609	99.6	309	5	ABG95159 Human GPC
4	1609	99.6	309	6	ABP82002 Human G p
5	1609	99.6	309	7	ADB67656 Human G p
6	1609	99.6	309	8	ADO29394 Human GPC
7	1609	99.6	309	8	ADO78094 Human GPC
8	1603	99.3	309	3	AAY69989 Human rec
9	1603	99.3	547	7	ADf70461 Orphan re
10	1601	99.1	309	7	ADf50511 Human GPC
11	1597	98.9	309	3	AAY58645 Human G-p
12	1597	98.9	309	6	ADA84069 Human GPR
13	1597	98.9	394	8	ADO78095 Human GPR
14	1597	98.9	394	8	ADR10454 Human pro
15	1377	85.3	286	8	ADP29765 Human sec
16	1123	69.5	307	8	ADO29395 Mouse GPC
17	401	24.8	370	2	Aaw62597 Human 7-t
18	401	24.8	370	5	ABP61511 Human NF-
19	401	24.8	370	6	ABG73513 Human p2y
20	401	24.8	370	6	ABP81870 Human G p
21	401	24.8	370	7	ADH69286 Human pur
22	401	24.8	370	8	ADf91778 Human p2y
23	401	24.8	370	8	ADO29049 Human nov
24	401	24.8	370	8	ADQ88244 Human 241
25	401	24.8	370	8	ADQ81575 Human 1ys

26	401	24.8	608	7	ADP70491 Orphan re
27	400	24.8	370	7	ADH69285 Human pur
28	400	24.8	370	8	ADf91777 Human p2y
29	396	24.5	370	8	ADO29050 Mouse nov
30	391	24.2	370	5	ABP61510 Human NF-
31	388	24.0	327	8	ADO29415 Mouse GPC
32	377.5	23.4	363	5	Aau77993 Human inf
33	377.5	23.4	363	5	ADJ63782 Human G p
34	377.5	23.4	363	7	ADf28998 Human G p
35	376.5	23.3	362	6	ABG72358 Human orp
36	376.5	23.3	363	2	Aaw94654 G-protein
37	376.5	23.3	363	4	Aau04379 Human G-p
38	376.5	23.3	363	7	ADC86215 Human GPC
39	376.5	23.3	363	7	ADL96482 Human G p
40	376.5	23.3	363	7	ADn38908 Cancer/an
41	376.5	23.3	363	8	ADM46118 Human 5-o
42	376.5	23.3	363	8	ADM46120 Human 5-o
43	376.5	23.3	363	8	ADn41887 Amino aci
44	376.5	23.3	363	8	ADO05575 Human hru
45	376.5	23.3	363	8	ADP04973 Human HM7

#### ALIGNMENTS

#### RESULT 1

ABG95172

ID ABG95172 standard; protein; 309 AA.

XX AC ABG95172;

XX DT 04-DEC-2002 (first entry)

XX DE Human GPCR GPR35 mutant A216K.

XX KW Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy;  
KW hypertension; reflux disease; depression; migraine; schizophrenia; ulcer;  
KW psychotic disorder; asthma; bronchospasm; anaesthesia;  
KW myocardial infarction; MI; stroke; glaucoma; anxiety;  
KW prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina;  
KW prostatic hypertrophy; receptor; mutant; mutein.

XX OS Homo sapiens.

OS Synthetic.

XX FN WO200268600-A2.

XX PD 06-SEP-2002.

XX 26-FEB-2002; 2002WO-US005625.

XX 26-FEB-2001; 2001US-0271913P.

XX (AREN-) ARENA PHARM INC.

XX Liaw CW, Chalmers DT, Behan DP, Maciejewski-Lenior D, Leonard JW;

XX Lin I, Ortuno D;

XX WPI; 2002-706980/76.

XX N-PSDB; ABS73401.

XX New human G-protein coupled receptor (GPCR), useful for screening agonist

XX or inverse agonist compounds for treating diseases associated with GPCR.

XX Example 2; Page 189-190; 201pp; English.

XX The present invention relates to transmembrane receptors, particularly  
XX endogenous human G-protein coupled receptors (GPCRs), mutant (non-  
XX endogenous) versions of the GPCRs, and the polynucleotide sequences  
XX encoding them. The GPCRs are useful for screening agonist or inverse  
XX agonist compounds for treating diseases associated with GPCR. Diseases  
XX that can be treated with such compounds include allergies, hypercension,  
XX reflux disease, depression, migraine, schizophrenia, ulcers, psychotic

CC disorders, asthma, bronchospasm, anaesthesia, myocardial infarction (MI),  
CC stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer,  
CC anxiety, prostatic hypertrophy, rhinitis, and angina. The present  
CC sequence represents a mutant human GPCR

XX SQ Sequence 309 AA;

Query Match 100.0%; Score 1615; DB 5; Length 309;  
Best Local Similarity 100.0%; Pred. No. 2.3e-168;  
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTPWPAIKLGFAYLGVLLVGLLLNSLALWVFCRQQTETRIYMT 60  
DB 1 MNGTYNTCGSSDLTPWPAIKLGFAYLGVLLVGLLLNSLALWVFCRQQTETRIYMT 60

QY 61 NLAVADCLLCTLPFVLSLRDTSPTPLCQLSQGIYLTNRYSISLVTAIVDRYVVRH 120  
DB 61 NLAVADCLLCTLPFVLSLRDTSPTPLCQLSQGIYLTNRYSISLVTAIVDRYVVRH 120

QY 121 PLRARGLRSPQAAACAVLWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLGLF 180  
DB 121 PLRARGLRSPQAAACAVLWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLGLF 180

QY 181 YLPLAVVVFCSLKVVTTALAQRPPTDVGQAEATRKAKRMVWVNLVVFVVCFLPLHVLTVR 240  
DB 181 YLPLAVVVFCSLKVVTTALAQRPPTDVGQAEATRKAKRMVWVNLVVFVVCFLPLHVLTVR 240

QY 241 LAVGNACALLETTIRRALYITSKLSDANCCLDIAICYYNMAKEFOEASALAVAPRAKAHKS 300  
DB 241 LAVGNACALLETTIRRALYITSKLSDANCCLDIAICYYNMAKEFOEASALAVAPRAKAHKS 300

QY 301 QDSLVCVTILA 309  
DB 301 QDSLVCVTILA 309

RESULT 2  
AAY79576  
ID AAY79576 standard; protein; 309 AA.

XX AC AAY79576;  
XX 15-AUG-2000 (first entry)  
XX Human G protein coupled receptor GPR35.

KW GPR35; G protein coupled receptor; human; NIDDM1;  
KW non-insulin-dependent diabetes mellitus; CAPN10 gene; calpain 10;  
KW diagnosis; therapy.

OS Homo sapiens.  
XX Key Location/Qualifiers  
FT Misc-difference 174 /note= "encoded by GCG"  
FT Misc-difference 234 /note= "encoded by AGT"  
FT FT  
XX WO200023603-A2.

XX 27-APR-2000.  
XX 21-OCT-1999; 99WO-US024890.  
XX 21-OCT-1998; 98US-0105052P.  
XX 13-MAY-1999; 99US-0134175P.  
XX (ARCH-) ARCH DEV CORP.  
XX (TEXA ) UNIV OF TEXAS SYSTEM.

XX Polonsky KS, Horikawa Y, Oda N, Sreenan S, Zhou Y, Otani K;  
XX Hanis CL, Bell GI, Cox NJ;  
XX

DR WPI; 2000-339702/29.  
XX N-PSDB; AAA27485, AAY79574, AAY79576.

XX Method for screening for type 2 diabetes mellitus comprises detecting a  
PT polymorphism in a calpain encoding nucleic acid segment or a protease-  
PT encoding nucleic acid segment.

XX Claim 75; Page 237-238; 257pp; English.

XX The present sequence is that of the human gene encoding G protein coupled  
CC receptor, GPR35 as deduced from a composite cDNA (see AAA27485). The  
CC sequence of GPR35 is similar to that of a putative purinoceptor P2Y9  
CC (34.1% identity) suggesting that ATP or other nucleotide is its ligand.  
CC GPR35 mRNA was detected in all adult and foetal tissues examined with  
CC relatively higher levels in adult lung, small intestine, colon and  
CC stomach. In these tissues, there are 2 major transcripts of 2.4 and 4.4  
CC kb, whereas in skeletal muscle there is a single transcript of 9.4 kb.  
CC The GPR35 gene is located in a 49,136 bp region (see AAA27475) within the  
CC NIDDM1 region of human chromosome 2. This region also includes the CAPN10  
CC gene, which encodes a novel calpain-like cysteine protease, designated  
CC calpain 10. Mutations in the CAPN10 gene are responsible for a  
CC susceptibility to type 2 diabetes. Claimed methods for screening for a  
CC propensity for type 2 diabetes mellitus are based on detection of a  
CC polymorphism in a calpain encoding nucleic acid. Methods are also claimed  
CC for identifying modulators of calpain activity, and using these  
CC modulators to treat diabetes, in particular through the regulation of an  
CC insulin secretory response or insulin mediated glucose transport

XX SQ Sequence 309 AA;

Query Match 99.6%; Score 1609; DB 3; Length 309;  
Best Local Similarity 99.7%; Pred. No. 1e-167;  
Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTPWPAIKLGFAYLGVLLVGLLLNSLALWVFCRQQTETRIYMT 60  
DB 1 MNGTYNTCGSSDLTPWPAIKLGFAYLGVLLVGLLLNSLALWVFCRQQTETRIYMT 60

QY 61 NLAVADCLLCTLPFVLSLRDTSPTPLCQLSQGIYLTNRYSISLVTAIVDRYVVRH 120  
DB 61 NLAVADCLLCTLPFVLSLRDTSPTPLCQLSQGIYLTNRYSISLVTAIVDRYVVRH 120

QY 121 PLRARGLRSPQAAACAVLWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLGLF 180  
DB 121 PLRARGLRSPQAAACAVLWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLGLF 180

QY 181 YLPLAVVVFCSLKVVTTALAQRPPTDVGQAEATRKAKRMVWVNLVVFVVCFLPLHVLTVR 240  
DB 181 YLPLAVVVFCSLKVVTTALAQRPPTDVGQAEATRKAKRMVWVNLVVFVVCFLPLHVLTVR 240

QY 241 LAVGNACALLETTIRRALYITSKLSDANCCLDIAICYYNMAKEFOEASALAVAPRAKAHKS 300  
DB 241 LAVGNACALLETTIRRALYITSKLSDANCCLDIAICYYNMAKEFOEASALAVAPRAKAHKS 300

QY 301 QDSLVCVTILA 309  
DB 301 QDSLVCVTILA 309

RESULT 3  
ABG95159  
ID ABG95159 standard; protein; 309 AA.  
XX AC ABG95159;

XX 04-DEC-2002 (first entry)  
XX Human GPCR GPR35.  
XX Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy;  
KW hypertension; reflux disease; depression; migraine; schizophrenia; ulcer;  
KW psychotic disorder; asthma; bronchospasm; anaesthesia;  
KW myocardial infarction; MI; stroke; glaucoma; anxiety;

KW prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina;  
 XX prostatic hypertrophy; receptor.  
 OS Homo sapiens.  
 XX WO200268600-A2.  
 XX 06-SEP-2002.  
 XX 26-FEB-2002; 2002WO-US005625.  
 XX 26-FEB-2001; 2001US-0271913P.  
 XX (AREN-) ARENA PHARM INC.  
 XX Liaw CW, Chalmers DT, Behan DP, Maciejewski-Lenior D, Leonard JN;  
 PI Lin I, Ortuno D;  
 XX  
 DR WPI; 2002-706980/76.  
 DR N-PSDB; ABS73345.  
 XX  
 PT New human G-protein coupled receptor (GPCR), useful for screening agonist  
 PT or inverse agonist compounds for treating diseases associated with GPCR.  
 XX  
 PS Claim 29; Page 128-130; 201pp; English.  
 XX  
 CC The present invention relates to transmembrane receptors, particularly  
 CC endogenous human G-protein coupled receptors (GPCRs), mutant (non-  
 CC endogenous) versions of the GPCRs, and the polynucleotide sequences  
 CC encoding them. The GPCRs are useful for screening agonist or inverse  
 CC agonist compounds for treating diseases associated with GPCR. Diseases  
 CC that can be treated with such compounds include allergies, hypertension,  
 CC reflux disease, depression, migraine, schizophrenia, ulcers, psychotic  
 CC disorders, asthma, bronchospasm, anaesthesia, myocardial infarction (MI),  
 CC stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer,  
 CC anxiety, prostatic hypertrophy, rhinitis, and angina. The present  
 CC sequence represents an endogenous human GPCR  
 XX  
 SQ Sequence 309 AA;

Query Match 99.6%; Score 1609; DB 5; Length 309;  
 Best Local Similarity 99.7%; Pred. No. 1e-167;  
 Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 NMGTYNTCGSSDLTPPPAIKLGFAVYLGVLVGLLLNSLALWVFCRQQTETRIYMT 60  
 Db 1 NMGTYNTCGSSDLTPPPAIKLGFAVYLGVLVGLLLNSLALWVFCRQQTETRIYMT 60  
 Qy 61 NLAVADLCCLCTLPVLSLSDTSPTPLCQLSQGIYLTNRNYSISLVTIAVDRIYVVRH 120  
 Db 61 NLAVADLCCLCTLPVLSLSDTSPTPLCQLSQGIYLTNRNYSISLVTIAVDRIYVVRH 120  
 Qy 121 PLRAGLRSRQAAVCAVLVLTGSLVARWLLGIQGGFCFSTRNENSMRPLLG 180  
 Db 121 PLRAGLRSRQAAVCAVLVLTGSLVARWLLGIQGGFCFSTRNENSMRPLLG 180  
 Qy 181 YLPLAVVVFCSIKVVTALAQRPPTDVGQAEATRKAKRVWVNLVVFVCFPLHVLTVR 240  
 Db 181 YLPLAVVVFCSIKVVTALAQRPPTDVGQAEATRKAKRVWVNLVVFVCFPLHVLTVR 240  
 Qy 241 LAVGNACALLETIRRALYITSKUSDANCCLDAICYYYMAKEFQASALAVAPRAKAHS 300  
 Db 241 LAVGNACALLETIRRALYITSKUSDANCCLDAICYYYMAKEFQASALAVAPRAKAHS 300  
 Qy 301 QDSLVCVTILA 309  
 Db 301 QDSLVCVTILA 309

## RESULT 4

ABP82002

ID ABP82002 standard; protein; 309 AA.

XX

AC ABP82002;  
 XX 04-MAR-2003 (first entry)  
 XX Human G protein-coupled receptor GPR35 protein SEQ ID NO:492.  
 XX  
 KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
 KW G protein-coupled receptor modulator; antibody; immune-related disease;  
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
 KW immunological-related cell proliferative disease; autoimmune disease;  
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
 KW ulcer.  
 XX Homo sapiens.  
 XX WO200261087-A2.  
 XX 08-AUG-2002.  
 XX 19-DEC-2001; 2001WO-US050107.  
 XX 19-DEC-2000; 2000US-0257144P.  
 XX (LIFE-) LIFESPAN BIOSCIENCES INC.  
 XX Burner GC, Roush CL, Brown JP;  
 XX WPI; 2003-046718/04.  
 XX N-PSDB; ABZ42852.  
 XX New isolated antigenic peptides e.g., for G protein-coupled receptors  
 XX (GPCR), useful for diagnosing and designing drugs for treating conditions  
 XX in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
 XX autoimmune diseases.  
 XX Disclosure; Fig 1; 523pp; English.  
 PS The present invention describes antigenic peptides (I) comprising: (a)  
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
 CC acids. Also described: (1) an assay for the detection of a particular G  
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
 CC and (2) an isolated antibody having high specificity and high affinity or  
 CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in  
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an  
 CC antibody against a particular GPCR, and in the production of specific  
 CC antibodies. The peptides and antibodies are also useful for detecting the  
 CC presence or absence of corresponding GPCRs. The antigenic peptides for  
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
 CC treating immune-related diseases, growth-related diseases, cell  
 CC regeneration-related disease, immunological-related cell proliferative  
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
 CC any other disorder in which GPCRs are involved. The antibodies may be  
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode  
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 309 AA;

## Query Match

Best Local Similarity 99.6%; Score 1609; DB 6; Length 309;

Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



```

QY      1  MNGTYNTCGSSDLTWPPPAIKLGFAYLGVLLVGLLLNSLALWVFCRMOQTETRIYMT 60
DB      1  MNGTYNTCGSSDLTWPPPAIKLGFAYLGVLLVGLLLNSLALWVFCRMOQTETRIYMT 60

QY     61  NLAVADLCLLCTLPFVLSLSDTSPTPLCQLSQGIYLTNRYSISLVTAIAVDRYVAVRH 120
DB     61  NLAVADLCLLCTLPFVLSLSDTSPTPLCQLSQGIYLTNRYSISLVTAIAVDRYVAVRH 120

QY    121  PLRAGRLSPRQAAAVCAVLVWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLGCF 180
DB    121  PLRAGRLSPRQAAAVCAVLVWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLGCF 180

QY    181  YLPLAVVVFCSLKVVYTAQAORPPTDVGQAETRAKRMVWNLVVFVVCFLPLHVGLTVR 240
DB    181  YLPLAVVVFCSLKVVYTAQAORPPTDVGQAETRAKRMVWNLVVFVVCFLPLHVGLTVR 240

QY    241  LAVGNACALLETIRRALYITSKLSANDCCDAICYYWMAKEFQASALAVAPRAKAHKS 300
DB    241  LAVGNACALLETIRRALYITSKLSANDCCDAICYYWMAKEFQASALAVAPRAKAHKS 300

QY    301  QDSLVCVTLA 309
DB    301  QDSLVCVTLA 309

```

## RESULT 5

ADB67656  
ID ADB67656 standard; protein; 309 AA.

AC ADB67656;

DT 04-DEC-2003 (first entry)

DE Human G protein-coupled receptor 35, SEQ ID 25.

DE Cardiant; Gene therapy; heart failure; human;

KW G protein-coupled receptor 35; receptor.

XX Homo sapiens.

XX WO2003072824-A1.

XX 04-SEP-2003.

XX 27-FEB-2003; 2003WO-JP002228.

XX 28-FEB-2002; 2002JP-00054388.

PR 15-APR-2002; 2002JP-00112228.

XX (SANY ) SANKYO CO LTD.

XX Kitakaze M, Takashima S, Asakura M, Isomura T, Furukawa H;

PI Koishi R, Nakamatsu K;

XX WPI; 2003-679959/64.

DR N-PSDB; ADB67672.

XX Predicting pathological conditions in heart failure using marker genes and proteins.

XX Claim 1; Page 111-113; 137pp; Japanese.

XX The present invention relates to a method for predicting pathological conditions in heart failure using expression of one of 17 gene sequences (ADB67663-ADB67678); or protein sequences encoded by the genes (ADB67648-ADB67662). The proteins and genes are useful for diagnosis, treatment and prevention of heart failure.

XX Sequence 309 AA;

Query Match 99.6%; Score 1609; DB 7; Length 309;

Best Local Similarity 99.7%; Pred. No. 1e-167;

```

Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      1  MNGTYNTCGSSDLTWPPPAIKLGFAYLGVLLVGLLLNSLALWVFCRMOQTETRIYMT 60
DB      1  MNGTYNTCGSSDLTWPPPAIKLGFAYLGVLLVGLLLNSLALWVFCRMOQTETRIYMT 60

QY     61  NLAVADLCLLCTLPFVLSLSDTSPTPLCQLSQGIYLTNRYSISLVTAIAVDRYVAVRH 120
DB     61  NLAVADLCLLCTLPFVLSLSDTSPTPLCQLSQGIYLTNRYSISLVTAIAVDRYVAVRH 120

QY    121  PLRAGRLSPRQAAAVCAVLVWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLGCF 180
DB    121  PLRAGRLSPRQAAAVCAVLVWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPPLGCF 180

QY    181  YLPLAVVVFCSLKVVYTAQAORPPTDVGQAETRAKRMVWNLVVFVVCFLPLHVGLTVR 240
DB    181  YLPLAVVVFCSLKVVYTAQAORPPTDVGQAETRAKRMVWNLVVFVVCFLPLHVGLTVR 240

QY    241  LAVGNACALLETIRRALYITSKLSANDCCDAICYYWMAKEFQASALAVAPRAKAHKS 300
DB    241  LAVGNACALLETIRRALYITSKLSANDCCDAICYYWMAKEFQASALAVAPRAKAHKS 300

QY    301  QDSLVCVTLA 309
DB    301  QDSLVCVTLA 309

```

## RESULT 6

ADO29394  
ID ADO29394 standard; protein; 309 AA.

XX ADO29394;

XX 29-JUL-2004 (first entry)

XX Human GPCR GPR35, SEQ ID NO:496.

XX G protein-coupled receptor; GPCR; drug screening; diagnosis;  
KW transgenic mouse; neurological disorder; adrenal gland disorder;  
KW colon disorder; intestinal disorder; cardiovascular disorder;  
KW muscular disorder; blood disorder; immune disorder; bone disorder;  
KW joint disorder; metabolic disorder; nutritive disorder; cancer;  
KW kidney disorder; liver disorder; lung disorder; breast disorder;  
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;  
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;  
KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;  
KW cytostatic; antiinflammatory; vasotropic; antidiarrhoeic; antidiabetic;  
KW CNS; central nervous system; respiratory; antidiarrhoeic; antiseborrhoeic;  
KW virucide; hepatotropic; antibacterial; antianaemic; anorectic;  
KW dermatological; antidiarrhoeic; antiallergic; anorectic;  
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;  
KW receptor.

XX Homo sapiens.

XX WO2004040000-A2.

XX 13-MAY-2004.

XX 09-SEP-2003; 2003WO-US028226.

XX 09-SEP-2002; 2002US-0409303P.

PR 09-APR-2003; 2003US-0461329P.

XX (PRIM-) PRIMAL INC.

XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;

PI Madisen L, Meilwain KL, Pavlova MN, Vassilatis D, Zeng H;

XX WPI; 2004-390329/36.

DR N-PSDB; ADO29916.

PT Novel mammalian G protein coupled receptors, useful for identifying





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Db      301 QDSLCTLA 309
RESULT 8
ID      AAY69989 standard; protein; 309 AA.
XX      AAY69989;
XX      AAY69989;
DT      31-MAY-2000 (first entry)
XX      Human receptor-associated protein from Incyte clone 3083742.
XX      Human receptor-associated protein; HRAP; Incyte clone 3083742;
KW      cytosolic; immunomodulatory; anti-inflammatory; cardiant; antianaemic;
KW      antiarteriosclerotic; hepatotropic; antiarthritic antirheumatic;
KW      antiasthmatic; osteopathic; antiallergic; antidiabetic; dermatological;
KW      neuroprotective; diagnosis; treatment; prevention; reproductive disorder;
KW      cardiovascular; cell proliferative; autoimmune; inflammatory; allergy;
KW      gastrointestinal; atherosclerosis; cirrhosis; leukaemia; cancer; AIDS;
KW      arthritis; anaemia; asthma; dermatitis; diabetes; osteoporosis;
KW      multiple sclerosis; irritable bowel syndrome.
XX      Homo sapiens.
XX      OS
FH      Key
FT      Location/Qualifiers
FT      Modified-site 2
FT      /note= "Potential N-glycosylation site"
FT      Modified-site 79
FT      /note= "Potential phosphorylation site"
FT      Modified-site 98
FT      /note= "Potential phosphorylation site"
FT      Region 102..118
FT      /label= Signature sequence
FT      /note= "G-protein coupled receptor"
FT      Modified-site 129
FT      /note= "Potential phosphorylation site"
FT      Modified-site 165
FT      /note= "Potential phosphorylation site"
FT      Modified-site 191
FT      /note= "Potential phosphorylation site"
FT      Modified-site 212
FT      /note= "Potential phosphorylation site"
FT      Modified-site 238
FT      /note= "Potential phosphorylation site"
FT      Modified-site 253
FT      /note= "Potential phosphorylation site"
FT      Modified-site 261
FT      /note= "Potential phosphorylation site"
XX      WO200008155-A2.
XX      17-FEB-2000.
XX      06-AUG-1999; 99WO-US017777.
XX      07-AUG-1998; 98US-0160065P.
XX      01-SEP-1998; 98US-0098703P.
XX      (INCY-) INCYTE PHARM INC.
XX      Hillman JL, Yue H, Lal P, Tang YT, Gorgone GA, Guegler KJ;
XX      Corley NC, Baughn MR;
XX      WPI; 2000-205710/18.
XX      N-PSDB; AA250891.
XX      New human receptor-associated proteins (HRAP) useful for the diagnosis,
XX      treatment and prevention of cell proliferative, autoimmune, inflammatory,
XX      reproductive, cardiovascular, and gastrointestinal disorders.
XX      Claim 1; Page 76; 99pp; English.
XX
CC      The present sequence is human receptor-associated protein (HRAP) from
CC      Incyte clone 3083742 obtained from OVARUN01 cDNA library. This sequence
CC      is expressed in haematopoietic/immune, gastrointestinal and reproductive
CC      tissues. HRAP has cytosolic, immunomodulatory, antiinflammatory,
CC      cardiant, antiarteriosclerotic, hepatotropic, antiarthritic,
CC      antirheumatic, osteopathic, antiallergic, antianaemic, antiasthmatic,
CC      antidiabetic, dermatological and neuroprotective activities. The present
CC      sequence is useful in the diagnosis, treatment and prevention of
CC      disorders associated with HRAP expression, especially cell proliferative,
CC      autoimmune/inflammatory, reproductive, cardiovascular and
CC      gastrointestinal disorders (e.g. atherosclerosis, cirrhosis, leukaemia,
CC      cancer, AIDS, arthritis, allergies, anaemia, asthma, dermatitis,
CC      diabetes, osteoporosis, multiple sclerosis and irritable bowel syndrome)
XX      Sequence 309 AA;
SQ
Query Match 99.3%; Score 1603; DB 3; Length 309;
Best Local Similarity 99.4%; Pred. No. 4.7e-167;
Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      1 MNGTYNTCGSSDLTPPAIKLGFAYLGVLLVGLLNSLALWVFCRMOQWTEIRIYMT 60
DB      1 MNGTYNTCGSSDLTPPAIKLGFAYLGVLLVGLLNSLALWVFCRMOQWTEIRIYMT 60
QY      61 NLAVADLCLLCTLPFVLSLSDTSLPLCQLSQGIYLTNRVMSISLVTALVADRVYVVRH 120
DB      61 NLAVADLCLLCTLPFVLSLSDTSLPLCQLSQGIYLTNRVMSISLVTALVADRVYVVRH 120
QY      121 PLRARGLSRQAAAVCAVLVVLVIGSLVRLWLLGIQEGGFCFRSTRHNFNSMRPFLG 180
DB      121 PLRARGLSRQAAAVCAVLVVLVIGSLVRLWLLGIQEGGFCFRSTRHNFNSMRPFLG 180
QY      181 YLPLAVVVFCSLKVVYVLTALVQRPPTDVGOAETRAKRWVWVNLVYVVCFLPLHVGLTVR 240
DB      181 YLPLAVVVFCSLKVVYVLTALVQRPPTDVGOAETRAKRWVWVNLVYVVCFLPLHVGLTVR 240
QY      241 LAVGNACALLETIRRALYITSKLSNDANCCLDALCYVYMAKEFOEASALAVAPRAKAKHS 300
DB      241 LAVGNACALLETIRRALYITSKLSNDANCCLDALCYVYMAKEFOEASALAVAPRAKAKHS 300
QY      301 QDSLCTLA 309
DB      301 QDSLCTLA 309
RESULT 9
ADF70461
ID      ADF70461 standard; protein; 547 AA.
XX      AC
XX      ADF70461;
XX      DT 12-FEB-2004 (first entry)
XX      DE
XX      Orphan receptor ligand-related human protein SeqID84.
XX      KW ligand; orphan receptor protein; fusion protein; fluorescent protein;
XX      KW cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFP;
XX      KW GFPuv; Enhanced GFP; EGFP; human.
XX      OS
XX      Homo sapiens.
XX      PN WO2003071272-A1.
XX      PD 28-AUG-2003.
XX      PF 21-FEB-2003; 2003WO-JP001901.
XX      PR 22-FEB-2002; 2002JP-00045728.
XX      PR 23-JUL-2002; 2002JP-00213949.
XX      PR 11-OCT-2002; 2002JP-00298237.
XX      PA (TAKE ) TAKEDA CHEM IND LTD.
XX

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PI Hinuma S, Fujii R, Ogi K, Komatsu H, Kawamata Y, Hosoya M;  
 XX WPI; 2003-697654/66.  
 DR N-PSDB; ADF70563.  
 XX  
 PT Transformation of cells with a fusion protein of an orphan receptor  
 PT protein with a fluorescent protein useful for identification of ligands  
 PT to the orphan receptor.  
 XX  
 XX Disclosure; SEQ ID NO 84; 594bp; Japanese.  
 PS  
 CC This invention relates to a novel method of identifying ligands to an  
 CC orphan receptor protein which comprises transforming cells with DNA  
 CC encoding a fusion protein of the orphan receptor with a fluorescent  
 CC protein, so that the fusion protein is expressed in the cells (or cell  
 CC membranes isolated from them) and contacting the cells with the potential  
 CC ligand to be tested. A suitable fluorescent protein for incorporation in  
 CC the fusion protein is green fluorescent protein (GFP), for example GFP-1,  
 CC wild-type GFP, GFPuv or Enhanced GFP (EGFP). The method is useful for the  
 CC identification of ligands binding to an orphan receptor protein.  
 XX  
 SQ Sequence 547 AA;  
 Query Match 99.3%; Score 1603; DB 7; Length 547;  
 Best Local Similarity 99.4%; Pred. No. 9.6e-167;  
 Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MNGYNTCGSSDLTPPPAIFGAYLGLVLLGLLNSLALWVFCRMOQWTEIRYMT 60  
 DB 1 MNGYNTCGSSDLTPPPAIFGAYLGLVLLGLLNSLALWVFCRMOQWTEIRYMT 60  
 QY 61 NLAVADLCCLCTLPVLSLSDTSPLCQLSQGIYLTNRYSISLVTAIADRVAVRH 120  
 DB 61 NLAVADLCCLCTLPVLSLSDTSPLCQLSQGIYLTNRYSISLVTAIADRVAVRH 120  
 QY 121 PLRAGLSRPRQAAAVCAVLWLVIGSLVARWLLGIQGGFCFRSTRNFNSMRPPLIGF 180  
 DB 121 PLRAGLSRPRQAAAVCAVLWLVIGSLVARWLLGIQGGFCFRSTRNFNSMRPPLIGF 180  
 QY 181 YLPLAVVVFCSLKVVTTALAQRPPTDVQAEATRKARVMWANLLVVFVCFPLHVLTVR 240  
 DB 181 YLPLAVVVFCSLKVVTTALAQRPPTDVQAEATRKARVMWANLLVVFVCFPLHVLTVR 240  
 QY 241 LAVGNACALLETIRRALYITSKLSDANCCCLDAICYYTMAKEFOEASALAVAPRAKHS 300  
 DB 241 LAVGNACALLETIRRALYITSKLSDANCCCLDAICYYTMAKEFOEASALAVAPRAKHS 300  
 QY 301 QDSLCTVTLA 309  
 DB 301 QDSLCTVTLA 309  
 RESULT 10  
 ADF50511  
 ID ADF50511 standard; protein; 309 AA.  
 XX  
 AC ADF50511;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Human GPCR GPR35 D113A mutein (SeqID 191).  
 DE  
 XX mutant; mutein; transformation; endocrine cell line;  
 KW expression cloning system; bioactive peptide; GPCR ligand; human.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 113  
 FT /note= "Wild type Asp substituted by Ala"  
 XX  
 PN WO2003087366-A1.

XX 23-OCT-2003.  
 PD  
 XX 16-APR-2003; 2003WO-JP004840.  
 PF  
 XX 16-APR-2002; 2002JP-00113030.  
 PR  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 PA  
 XX Sasaki K, Miura K, Saeki S, Yoshizawa M, Kishimoto K, Kunitomo H;  
 PI Nishi T, Obinata M;  
 PI WPI; 2003-833737/77.  
 DR  
 XX Endocrine cell lines originated from mammalian hypothalamus and  
 PT pancreatic islet, applicable in expression cloning systems of bioactive  
 PT peptide precursor genes, and in screening G protein-coupled receptor  
 PT ligands.  
 PT  
 XX Example 24; SEQ ID NO 191; 316pp; Japanese.  
 PS  
 XX This invention relates to a novel method for obtaining a DNA that encodes  
 CC a peptide acting as agonist, antagonist or inverse agonist on a target  
 CC receptor. Specifically, it comprises transformation of endocrine cell  
 CC lines originating from mammalian hypothalamus and pancreatic islets,  
 CC culturing the transformants and contacting with cells expressing the  
 CC target receptor. The identification of those cells with a response  
 CC reaction can be used for selecting a transformant cell line with the  
 CC appropriate target activity that is expressing the novel transformed DNA.  
 CC Accordingly, the present invention describes novel cell lines that are  
 CC applicable in expression cloning systems of bioactive peptide precursor  
 CC genes, and in screening GPCR ligands for use as drugs including agonists,  
 CC antagonists and inverse agonists i.e. activators and inhibitors. Such  
 CC cell lines can provide a highly sensitive and convenient GPCR ligand  
 CC assay system. This polypeptide sequence is the human GPCR GPR35 D113A  
 CC mutein of the invention.  
 XX  
 SQ Sequence 309 AA;  
 Query Match 99.1%; Score 1601; DB 7; Length 309;  
 Best Local Similarity 99.4%; Pred. No. 7.8e-167;  
 Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 MNGYNTCGSSDLTPPPAIFGAYLGLVLLGLLNSLALWVFCRMOQWTEIRYMT 60  
 DB 1 MNGYNTCGSSDLTPPPAIFGAYLGLVLLGLLNSLALWVFCRMOQWTEIRYMT 60  
 QY 61 NLAVADLCCLCTLPVLSLSDTSPLCQLSQGIYLTNRYSISLVTAIADRVAVRH 120  
 DB 61 NLAVADLCCLCTLPVLSLSDTSPLCQLSQGIYLTNRYSISLVTAIADRVAVRH 120  
 QY 121 PLRAGLSRPRQAAAVCAVLWLVIGSLVARWLLGIQGGFCFRSTRNFNSMRPPLIGF 180  
 DB 121 PLRAGLSRPRQAAAVCAVLWLVIGSLVARWLLGIQGGFCFRSTRNFNSMRPPLIGF 180  
 QY 181 YLPLAVVVFCSLKVVTTALAQRPPTDVQAEATRKARVMWANLLVVFVCFPLHVLTVR 240  
 DB 181 YLPLAVVVFCSLKVVTTALAQRPPTDVQAEATRKARVMWANLLVVFVCFPLHVLTVR 240  
 QY 241 LAVGNACALLETIRRALYITSKLSDANCCCLDAICYYTMAKEFOEASALAVAPRAKHS 300  
 DB 241 LAVGNACALLETIRRALYITSKLSDANCCCLDAICYYTMAKEFOEASALAVAPRAKHS 300  
 QY 301 QDSLCTVTLA 309  
 DB 301 QDSLCTVTLA 309  
 RESULT 11  
 AAY58645  
 ID AAY58645 standard; protein; 309 AA.  
 XX  
 AC AAY58645;

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XX 11-APR-2000 (first entry)
XX Human G-protein coupled receptor GPR35A.
XX GPR35A; human; G-protein coupled receptor; purinergic;
XX 7-transmembrane receptor; antibiotic; antifungal; antiviral; analgesic;
XX cytostatic; antidiabetic; anorectic; antischismatic; antiparkinsonian;
XX hypertensive; hypertensive; osteopathic; antianginal; cardiac;
XX cerebroprotective; antiulcer; antiallergic; antimigraine; antienetic;
XX tranquilizer; antidepressant; neuroleptic; nootropic; anticonvulsant;
XX therapy; diagnosis; vaccine.
XX Homo sapiens.
XX ADA84069
XX WO9964452-A1.
XX
XX 16-DEC-1999.
XX
XX 01-JUN-1999; 99WO-US012123.
XX
XX 11-JUN-1998; 98US-00096031.
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX Elshourbagy NA;
XX
XX WPI; 2000-116525/10.
XX N-PSDB; AA235390.
XX
XX New human GPR35A polypeptides and polynucleotides used to identify
XX agonists, antagonists and inhibitors for use in therapy.
XX
XX Claim 1; Page 32-33; 38pp; English.
XX
XX The present sequence represents human GPR35A, a novel member of the
XX purinergic family of polypeptides and a G-protein coupled receptor. The
XX invention provides GPR35A polypeptides having at least 70% identity with
XX the present sequence, GPR35A polynucleotides, recombinant materials, and
XX methods for their production. GPR35A polypeptides can be used for
XX identifying agonists and antagonists/inhibitors, and for detecting
XX diseases associated with inappropriate GPR35A activity or levels. GPR35A
XX polypeptides and polynucleotides, agonists, antagonists and antibodies
XX are used to treat infections such as bacterial, fungal, protozoan and
XX viral infections, particularly HIV-1 and HIV-2; pain; cancer; diabetes;
XX obesity; anorexia; bulimia; asthma; Parkinson's disease; acute heart
XX failure; hypotension; hypertension; urinary retention; osteoporosis;
XX angina pectoris; myocardial infarction; stroke; ulcers; allergy; benign
XX prostatic hypertrophy; migraine; vomiting; psychotic and neurological
XX disorders including anxiety, schizophrenia, manic depression, depression,
XX delirium, dementia and severe mental retardation; and dyskinesias such as
XX Huntington's or Gilles de la Tourette's syndrome. The polypeptide is also
XX useful for production of vaccines
XX
XX Sequence 309 AA;
XX
XX Query Match 98.9%; Score 1597; DB 3; Length 309;
XX Best Local Similarity 99.0%; Pred. No. 2.1e-166;
XX Matches 306; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1 MNGTYNTCCSSDLTPPAIKLGFAYLVGLVLLGLLNSLALWVFCRMOQNTETRIYMT 60
XX |||||||
XX 1 MNGTYNTCCSSDLTPPAIKLGFAYLVGLVLLGLLNSLALWVFCRMOQNTETRIYMT 60
XX |||||||
XX 61 NLAVADCLLCTLPFVHLSLRDTSPTPLCQLSGQIYLTNRYMSISLVAIAVDYVAVRH 120
XX |||||||
XX 61 NLAVADCLLCTLPFVHLSLRDTSPTPLCQLSGQIYLTNRYMSISLVAIAVDYVAVRH 120
XX |||||||
XX 121 PLRARGLRSPRAAAVCAVLWLVIGSLVARMVLGTOEGGFCFRSTRHFNFSMRPFLG 180
XX |||||||
XX 121 PLRARGLRSPRAAAVCAVLWLVIGSLVARMVLGTOEGGFCFRSTRHFNFSMRPFLG 180
XX |||||||
XX 181 YLPLAVVVFCSLKVVTALAQRPTDVGQAEATRKAKRMVWVANLLVFVVCFLPHVGLTVR 240
XX |||||||

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Db 181 YLPLAVVVFCSLKVVTALAQRPTDVGQAEATRKAKRMVWVANLLVFVVCFLPHVGLTVR 240
|||
Qy 241 LAVGNACALLETIRRALYITSKLSDANCCLDAICYTYMAKEFOESALAVAPRAKHS 300
|||
Db 241 LAVGNACALLETIRRALYITSKLSDANCCLDAICYTYMAKEFOESALAVAPRAKHS 300
|||
Qy 301 QDSLCLVTILA 309
|||
Db 301 QDSLCLVTILA 309
|||

RESULT 12
ADA84069
ID ADA84069 standard; protein; 309 AA.
XX
XX ADA84069;
XX
XX 20-NOV-2003 (first entry)
XX Human GPR35 protein.
XX
XX human; marker; expressed sequence tag; EST; arabidopsis; tumour;
XX stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;
XX vaccine.
XX
XX Homo sapiens.
XX
XX WO2002103028-A2.
XX
XX 27-DEC-2002.
XX
XX 30-MAY-2002; 2002WO-IB004189.
XX
XX 30-MAY-2001; 2001US-0293999P.
XX 22-OCT-2001; 2001US-0330457P.
XX 19-FEB-2002; 2002US-0357144P.
XX
XX (BIOM-) BIOMEDICAL CENT.
XX
XX Baranova AV, Yankovsky NK, Kozlov AP, Lobashev AV, Krukovskaya LL;
XX WPI; 2003-175241/17.
XX N-PSDB; ADA84068.
XX
XX Determining if a nucleic acid is a marker for a phenotype/cell type of
XX interest, by global comparison of expressed sequence tags known to be
XX expressed in the phenotype/cell type with all ESTs expressed in normal
XX tissue.
XX
XX Claim 29; Page 448-449; 516pp; English.
XX
XX The invention relates to a novel method for determining if a nucleic acid
XX is a marker for a predetermined phenotype/cell type of interest from a
XX biological species. The method comprises performing a global comparison
XX of a group of expressed sequence tags (ESTs) known to be expressed in the
XX phenotype/cell type of interest with all ESTs expressed in normal tissue
XX in order to identify ESTs that are preferentially expressed in the
XX phenotype/cell of interest. A method of the invention is useful for
XX determining whether a nucleic acid is a marker for a predetermined
XX phenotype or cell type of interest from a biological species, preferably
XX Arabidopsis or human. The cell type of interest is an abnormal cell such
XX as a tumour cell, and the predetermined phenotype is a stress-induced
XX phenotype such as hyperosmotic stress or high salt conditions. A method
XX of the invention is also useful for determining the progression of colon
XX cancer in a human, for detecting a tumour cell, and for regulating or
XX preventing the growth of a tumour cell. An antibody of the invention is
XX useful for detecting the absence or presence of peptides encoded by
XX tumour-associated markers. A polypeptide of the invention is useful as an
XX immunogen for vaccinating an animal. The present sequence represents a
XX tumour-associated antigen of the invention.
XX
XX Sequence 309 AA;
XX

```

Query Match 98.9%; Score 1597; DB 6; Length 309;  
 Best Local Similarity 99.0%; Pred. No. 2.1e-166;  
 Matches 306; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTWPPPAIKLGFYAYLVGLVLLGLLLNSLALWVFCRMOQWTETRIYMT 60  
 DB 1 MNGTYNTCGSSDLTWPPPAIKLGFYAYLVGLVLLGLLLNSLALWVFCRMOQWTETRIYMT 60

QY 61 NLAVADLCCLCTLPFVLSLSDTSTPLCQLSQGIYLTNRNYSISLVTAIAVDRYAVVRH 120  
 DB 61 NLAVADLCCLCTLPFVLSLSDTSTPLCQLSQGIYLTNRNYSISLVTAIAVDRYAVVRH 120

QY 121 PLRARGLSRPRQAAACAVLWLVLTGSLVARWLLGIQEGGFCFRSTRNFNSMRPFLIGF 180  
 DB 121 PLRARGLSRPRQAAACAVLWLVLTGSLVARWLLGIQEGGFCFRSTRNFNSMRPFLIGF 180

QY 181 YLPLAVVVFCSLKVVTTALAQRPTDVGQAEATRKAKRMVWNLVVFVCFPLPHVGLTVR 240  
 DB 181 YLPLAVVVFCSLKVVTTALAQRPTDVGQAEATRKAKRMVWNLVVFVCFPLPHVGLTVR 240

QY 241 LAVGNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQASALAVAPRAKAHKS 300  
 DB 241 LAVGNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQASALAVAPRAKAHKS 300

QY 301 QDSLCTVTLA 309  
 DB 301 QDSLCTVTLA 309

RESULT 13  
 ADO78095  
 ID ADO78095 standard; protein; 394 AA.  
 XX AC ADO78095;  
 XX XX  
 DT 26-AUG-2004 (first entry)  
 DE Human GPR35 isoform.  
 XX  
 KW tumour-associated antigen; TAG; cancer; lung cancer; breast cancer;  
 KW prostate cancer; colon cancer; stomach cancer; pancreatic cancer;  
 KW ear cancer; nose cancer; throat cancer; kidney cancer; cervical cancer;  
 KW melanoma; tumour; human; GPR35.  
 XX  
 OS Homo sapiens.  
 XX  
 PN DE10254601-A1.  
 XX  
 PD 03-JUN-2004.  
 XX  
 PF 22-NOV-2002; 2002DE-01054601.  
 XX  
 PR 22-NOV-2002; 2002DE-01054601.  
 XX  
 PA (GANY-) GANYMED PHARM AG.  
 XX  
 PI Tuereci O, Sahin U, Koslowski M;  
 XX  
 XX WPI; 2004-421820/40.  
 DR  
 XX  
 XX Composition containing inhibitor of expression or activity of specific  
 PT tumor-associated antigens, useful for treating cancers, also related  
 PT compositions for diagnosis and monitoring.  
 XX  
 PS Claim 72; SEQ ID NO 10; 124pp; German.  
 XX  
 CC The invention relates to pharmaceutical compositions that comprise an  
 CC agent that inhibits the expression or activity of a tumour-associated  
 CC antigen (TAG) that is encoded by a nucleic acid. The pharmaceutical  
 CC compositions and related compositions, are used for treatment of diseases  
 CC associated with (abnormal) expression of TAG, specifically cancer e.g. of  
 CC lung, breast, prostate, colon, stomach, pancreas, ear/nose/throat, kidney

CC or cervix, also melanoma. Compositions containing TAG, or related nucleic  
 CC acid, antibodies or host cells, are also useful for diagnosis and  
 CC monitoring of tumours. The present sequence represents the amino acid  
 CC sequence of a human GPR35.  
 XX  
 SQ Sequence 394 AA;

Query Match 98.9%; Score 1597; DB 8; Length 394;  
 Best Local Similarity 99.0%; Pred. No. 2.9e-166;  
 Matches 306; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTWPPPAIKLGFYAYLVGLVLLGLLLNSLALWVFCRMOQWTETRIYMT 60  
 DB 86 MNGTYNTCGSSDLTWPPPAIKLGFYAYLVGLVLLGLLLNSLALWVFCRMOQWTETRIYMT 145

QY 61 NLAVADLCCLCTLPFVLSLSDTSTPLCQLSQGIYLTNRNYSISLVTAIAVDRYAVVRH 120  
 DB 146 NLAVADLCCLCTLPFVLSLSDTSTPLCQLSQGIYLTNRNYSISLVTAIAVDRYAVVRH 205

QY 121 PLRARGLSRPRQAAACAVLWLVLTGSLVARWLLGIQEGGFCFRSTRNFNSMRPFLIGF 180  
 DB 206 PLRARGLSRPRQAAACAVLWLVLTGSLVARWLLGIQEGGFCFRSTRNFNSMRPFLIGF 265

QY 181 YLPLAVVVFCSLKVVTTALAQRPTDVGQAEATRKAKRMVWNLVVFVCFPLPHVGLTVR 240  
 DB 266 YLPLAVVVFCSLKVVTTALAQRPTDVGQAEATRKAKRMVWNLVVFVCFPLPHVGLTVR 325

QY 241 LAVGNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQASALAVAPRAKAHKS 300  
 DB 326 LAVGNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFQASALAVAPRAKAHKS 385

QY 301 QDSLCTVTLA 309  
 DB 386 QDSLCTVTLA 394

RESULT 14  
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 ID ADR10454 standard; protein; 394 AA.  
 XX AC ADR10454;  
 XX XX  
 DT 04-NOV-2004 (first entry)  
 XX  
 DE Human protein useful for treating neurological disease Seq 3960.  
 XX  
 KW human; oligo-capping method; diagnostic marker; gene therapy;  
 KW osteoporosis; neurological disease; Alzheimer's disease;  
 KW Parkinson's disease; dementia; short memory; cancer;  
 KW sense or motor function; emotional reaction; fear response; panic;  
 KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;  
 KW tranquiliser.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1447413-A2.  
 XX  
 PD 18-AUG-2004.  
 XX  
 XX 12-FEB-2004; 2004EP-00003145.  
 PF  
 XX  
 PR 14-FEB-2003; 2003JP-00102207.  
 PR  
 PR 09-MAY-2003; 2003JP-00131452.  
 XX  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 XX  
 XX Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;  
 PI Wakamatsu A, Ishii S, Nagai K, Irie R;  
 XX  
 XX WPI; 2004-583265/57.  
 DR  
 DR N-PSDB; ADR10415.  
 XX  
 XX New 1995 cDNA, useful for treating osteoporosis, neurological diseases,

PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.  
XX Claim 1; SEQ ID NO 3960; 2686pp; English.

XX This invention relates to novel, isolated full length human cDNA  
CC molecules and the encoded proteins thereof. Specifically, it refers to  
CC cDNA clones obtained by an oligo-capping method, where none of these  
CC clones are identical to any known human mRNAs. The present invention  
CC describes an immunoassay to identify agonists and antagonists, as well as  
CC antibodies, antisense molecules and siRNAs that can all be used to bind  
CC to and modulate expression of the cDNA molecules. As such, these  
CC molecules are useful for diagnostic markers or therapeutic targets for  
CC the various diseases or morbid states. In particular, they are useful in  
CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's  
CC disease, Parkinson's disease, dementia, short memory and various cancers,  
CC as well as for maintaining equilibrium of sense or motor function, and  
CC for treating emotional reaction, fear response and panic. Accordingly,  
CC they exhibit osteopathic, neuroprotective, neurotropic, antiparkinsonian,  
CC cytotatic and tranquiliser activities. This polypeptide is a protein  
CC encoded by a full length human cDNA sequence of the invention. NOTE: This  
CC sequence is not given in the sequence listing of the specification but  
CC can be obtained on CD-ROM from the European Patent Office, Vienna Sub-  
XX office.

SQ Sequence 394 AA;

Query Match 98.9%; Score 1597; DB 8; Length 394;  
Best Local Similarity 99.0%; Pred. No. 2.9e-166;  
Matches 306; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 MNGTYNTCGSSDLTPWPAIKLGFYALGVLLVGLLLSLALWVFCRMOQWTETRIYMT 60  
DB 86 MNGTYNTCGSSDLTPWPAIKLGFYALGVLLVGLLLSLALWVFCRMOQWTETRIYMT 145  
  
QY 61 NLAVADLCLLCTLPFVHLSDRTSDTLPQLSQGIYLTNRYSISLVTAIAVDYRVAVRH 120  
DB 146 NLAVADLCLLCTLPFVHLSDRTSDTLPQLSQGIYLTNRYSISLVTAIAVDYRVAVRH 205  
  
QY 121 PLRAGRLSPROAAVCAVLVLTGSLVARWLLGTOEGGFCFRSTRNFNSMRPFLG 180  
DB 206 PLRAGRLSPROAAVCAVLVLTGSLVARWLLGTOEGGFCFRSTRNFNSMAFPFLG 265  
  
QY 181 YLPLAVVVFCSLKVVTAQAORPTDVGAETRKAKRMVWNLVFCFLPHVGLTVR 240  
DB 266 YLPLAVVVFCSLKVVTAQAORPTDVGAETRKAKRMVWNLVFCFLPHVGLTVR 325  
  
QY 241 LAVGNACALLETRIRALYITSKLSDANCCLDIAICYVMKFEQASALAVAPRAKHS 300  
DB 326 LAVGNACALLETRIRALYITSKLSDANCCLDIAICYVMKFEQASALAVAPRAKHS 385  
  
QY 301 QBSLCVTLA 309  
DB 386 QBSLCVTLA 394

RESULT 15  
ADP29765  
ID ADP29765 standard; protein; 286 AA.

XX AC ADP29765;  
XX DT 12-AUG-2004 (first entry)  
XX DE Human secreted protein SEQ ID #532.  
XX KW Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;  
XX KW cancer; inflammatory; immune; human secreted protein.  
XX OS Homo sapiens.  
XX PN WO2004035732-A2.  
XX DT 29-APR-2004.

XX 28-AUG-2003; 2003WO-US026780.  
XX 29-AUG-2002; 2002US-0406576P.  
PR 29-AUG-2002; 2002US-0406579P.  
PR 29-AUG-2002; 2002US-0406585P.  
PR 29-AUG-2002; 2002US-0406588P.  
PR 29-AUG-2002; 2002US-0406608P.  
PR 29-AUG-2002; 2002US-0406611P.  
PR 29-AUG-2002; 2002US-0406612P.  
PR 29-AUG-2002; 2002US-0406616P.  
PR 29-AUG-2002; 2002US-0406640P.  
PR 29-AUG-2002; 2002US-0406642P.  
PR 29-AUG-2002; 2002US-0406653P.  
PR 29-AUG-2002; 2002US-0406655P.  
PR 29-AUG-2002; 2002US-0406666P.  
PR 17-SEP-2002; 2002US-0410946P.  
PR 17-SEP-2002; 2002US-0410947P.  
PR 17-SEP-2002; 2002US-0410948P.  
PR 17-SEP-2002; 2002US-0410949P.  
PR 17-SEP-2002; 2002US-0410953P.  
PR 17-SEP-2002; 2002US-0410957P.  
PR 17-SEP-2002; 2002US-0410958P.  
PR 17-SEP-2002; 2002US-0410959P.  
PR 17-SEP-2002; 2002US-0410960P.  
PR 17-SEP-2002; 2002US-0410961P.  
PR 17-SEP-2002; 2002US-0410962P.  
PR 17-SEP-2002; 2002US-0411019P.  
PR 17-SEP-2002; 2002US-0411022P.  
PR 17-SEP-2002; 2002US-0411023P.  
PR 17-SEP-2002; 2002US-0411024P.  
PR 17-SEP-2002; 2002US-0411032P.  
PR 17-SEP-2002; 2002US-0411035P.  
PR 17-SEP-2002; 2002US-0411037P.  
PR 17-SEP-2002; 2002US-0411041P.  
PR 17-SEP-2002; 2002US-0411045P.  
PR 17-SEP-2002; 2002US-0411046P.  
PR 17-SEP-2002; 2002US-0411048P.  
PR 17-SEP-2002; 2002US-0411052P.  
PR 17-SEP-2002; 2002US-0411055P.  
PR 17-SEP-2002; 2002US-0411073P.  
PR 17-SEP-2002; 2002US-0411082P.  
PR 17-SEP-2002; 2002US-0411101P.  
PR 17-SEP-2002; 2002US-0411111P.  
PR 18-APR-2003; 2003US-0463700P.  
PR 18-APR-2003; 2003US-0463708P.  
PR 18-APR-2003; 2003US-0463716P.  
PR 18-APR-2003; 2003US-0463732P.  
PR 02-MAY-2003; 2003US-0467199P.  
PR 02-MAY-2003; 2003US-0467201P.  
PR 02-MAY-2003; 2003US-0467203P.  
PR 02-MAY-2003; 2003US-0467205P.  
PR 19-MAY-2003; 2003US-0471306P.  
PR 19-MAY-2003; 2003US-0471336P.  
PR 22-MAY-2003; 2003US-0472420P.  
PR 22-MAY-2003; 2003US-0472430P.  
PR 09-JUN-2003; 2003US-0476609P.  
PR 09-JUN-2003; 2003US-0476641P.  
PR 08-JUL-2003; 2003US-0485218P.  
PR 08-JUL-2003; 2003US-0485223P.  
PR 08-JUL-2003; 2003US-0485224P.  
PR 08-JUL-2003; 2003US-0485325P.  
PR 14-JUL-2003; 2003US-0486446P.  
PR 14-JUL-2003; 2003US-0486480P.  
PR 15-JUL-2003; 2003US-0486891P.  
PR 15-JUL-2003; 2003US-0486960P.  
PR 08-AUG-2003; 2003US-0493341P.  
PR 08-AUG-2003; 2003US-0493370P.  
PR 08-AUG-2003; 2003US-0493573P.  
PR 08-AUG-2003; 2003US-0493577P.

(FIVE-) FIVE PRIME THERAPEUTICS INC.

XX PA

XX Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;  
PI Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;  
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;  
XX WPI; 2004-348438/32.  
DR  
XX  
PT New nucleic acid molecule for diagnosing, preventing or treating diseases  
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,  
PT genetic, bacterial and viral diseases.  
XX  
PS Claim 1; SEQ ID NO 1763; 428pp; English.  
XX  
CC The present invention relates to an isolated nucleic acid molecule  
CC encoding a polypeptide which is believed to be cytostatic,  
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The  
CC composition and methods are useful for diagnosing, preventing and  
CC treating diseases such as proliferative (e.g. cancer), inflammatory,  
CC immune, metabolic, genetic, bacterial and viral diseases. The present  
CC sequence represents a human secreted protein. The present sequence is  
CC available on WIPWEB and is not in the specification.  
XX  
SQ Sequence 286 AA;  
  
Query Match 85.3%; Score 1377; DB 8; Length 286;  
Best Local Similarity 99.2%; Pred. No. 2.8e-142;  
Matches 264; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
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DB 1 MNGYNTCGSSDLTWPPAIKLGFYALGVLLVGLLNSLALWVFCRMOQTETRIYMT 60  
  
QY 61 NLAVADLCCLCTLPFVLSLRDSTPLCQLSQGIYLTNRYSISLVTAIADVRYAVRH 120  
DB 61 NLAVADLCCLCTLPFVLSLRDSTPLCQLSQGIYLTNRYSISLVTAIADVRYAVRH 120  
  
QY 121 PLRAGLRSPQAAAVCAVLWVIGSLVARWLLGIQEGGCFRSTRNFNSMRPPLIGF 180  
DB 121 PLRAGLRSPQAAAVCAVLWVIGSLVARWLLGIQEGGCFRSTRNFNSMRPPLIGF 180  
  
QY 181 YLPLAVVVFCSLKVVTTALAQRPPTDVGQAEATRKAKRMWVANLLVFVVCFLPHVGLTVR 240  
DB 181 YLPLAVVVFCSLKVVTTALAQRPPTDVGQAEATRKAKRMWVANLLVFVVCFLPHVGLTVR 240  
  
QY 241 LAVGNACALLETIRRALYITSKLSD 266  
DB 241 LAVGNACALLETIRRALYITSKLSD 266

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Job time : 64 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
9480.388 Million cell updates/sec

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Perfect score: 930  
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Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	736.4	79.2	876	CN834209	CN834209 AGENCOURT
C 3	674.2	72.5	906	CN835542	CN835542 AGENCOURT
C 4	609.8	65.6	960	CN843697	CN843697 AGENCOURT
C 5	601.2	64.6	750	C0921772	C0921772 AGENCOURT
C 6	591.2	63.6	642	AY401608	AY401608 Pan trogl
C 7	581.8	62.6	778	C0923163	C0923163 AGENCOURT
C 8	571	61.4	759	C0957219	C0957219 AGENCOURT
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C 10	549.2	59.1	2849	AK036503	AK036503 Mus muscu
C 11	544.4	58.5	3158	AK034870	AK034870 Mus muscu
C 12	538.2	57.9	4254	AK089198	AK089198 Mus muscu
C 13	531.2	57.1	783	CN835586	CN835586 AGENCOURT
C 14	516.6	55.5	717	C0923285	C0923285 AGENCOURT
C 15	512.6	55.1	1019	CN832122	CN832122 AGENCOURT
C 16	510.6	54.9	777	C0921660	C0921660 AGENCOURT
C 17	510.4	54.9	1009	BB609892	BB609892 AGENCOURT
C 18	499.2	53.7	855	CN832152	CN832152 AGENCOURT
C 19	458	49.2	592	BM772486	BM772486 K-EST0056
C 20	415	44.6	827	CN843490	CN843490 AGENCOURT
C 21	392.6	42.2	614	BZ221309	BZ221309 CH230-312
C 22	374.4	40.3	690	BY747772	BY747772 BY747772
C 23	374.4	40.3	701	BY748928	BY748928 BY748928
C 24	338.4	36.4	372	BF766676	BF766676 CM3-CS004

C 25	335.4	36.1	736	1	AI861901	AI861901 td17f02.x
C 26	317.6	34.2	444	2	AW854188	AW854188 RC3-CT025
C 27	317	34.1	429	2	AW854178	AW854178 RC3-CT025
C 28	317	34.1	668	2	BB629414	BB629414 BB629414
C 29	313.4	33.7	648	7	C0957232	C0957232 AGENCOURT
C 30	308	33.1	457	2	AW854180	AW854180 RC3-CT025
C 31	307.4	33.1	616	2	BF151947	BF151947 u222c12.y
C 32	307	33.0	554	2	BE696076	BE696076 RC3-CT025
C 33	305.6	32.9	351	2	AW854187	AW854187 RC3-CT025
C 34	300.8	32.3	448	2	AW854198	AW854198 RC3-CT025
C 35	297.4	32.0	437	2	AW854203	AW854203 RC3-CT025
C 36	296	31.8	411	2	AW854204	AW854204 RC3-CT025
C 37	296	31.8	571	2	BE696051	BE696051 RC3-CT025
C 38	293.4	31.5	459	2	AW854197	AW854197 RC3-CT025
C 39	293.4	31.5	701	6	CB321988	CB321988 UI-CF-FNO
C 40	293	31.5	585	2	AW854051	AW854051 RC3-CT025
C 41	290.6	31.2	368	2	BF764582	BF764582 CM3-CS004
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C 43	285.6	30.7	325	2	BF764700	BF764700 CM3-CS004
C 44	282.8	30.4	428	2	AW854200	AW854200 RC3-CT025
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ALIGNMENTS

RESULT 1  
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LOCUS  
DEFINITION Homo sapiens GPR35 gene, VIRTUAL TRANSCRIPT, partial sequence,  
AY401607  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
ORIGIN

930 bp DNA linear GSS 15-DBC-2003

AY401607 Homo sapiens GPR35 gene, VIRTUAL TRANSCRIPT, partial sequence,  
Genomic survey sequence.  
AY401607.1 GI:39757596  
GSS.  
Homo sapiens (human)  
Homo sapiens  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 930)  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,  
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D. and Cargill, M.  
Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
Science 302 (5652), 1960-1963 (2003)  
14671302  
2 (bases 1 to 930)  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,  
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D. and Cargill, M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
Location/Qualifiers  
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/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
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/gene="GPR35"  
/locus\_tag="HCM0947"

Query Match 99.1%; Score 922; DB 9; Length 930;  
Best Local Similarity 99.5%; Pred. No. 4.6e-191;  
Matches 925; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
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QY 300 GTACATGAGCATCAGCTGCTCACGGCCATCGCGTGGACCGCTATGTGGCCGTGGGCA 359  
Db 668 GTACATAGGATCAGCTTGGTCAAGCCATCGCGGGAACCGTATGTGNCCTGGCCCA 609  
QY 360 CCCGCTGCTGCTGCGCGGCTGCGGTCCCGCAGGAGGCTGGCGGCTGTGGCGGCTCT 419  
Db 608 CCCGCTGCTGCTGCGCGGCTGCGGTCCCGCAGGAGGCTGGCGGCTGTGGCGGCTCT 549  
QY 420 CTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 479  
Db 548 CTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 489  
QY 480 CTCTCTGCTTACGAGACCCGACCAATTTCAACTCCATGCGGTTCCTGGGATT 539  
Db 488 CTCTCTGCTTACGAGACCCGACCAATTTCAACTCCATGCGGTTCCTGGGATT 429  
QY 540 CTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 599  
Db 428 CTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 369  
QY 600 GAGGCCACCCACGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 659  
Db 368 GAGGCCACCCACGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 309  
QY 660 GSCCAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 719  
Db 308 GSCCAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 249  
QY 720 CTTCCAGTGGGCTGGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 779  
Db 248 CTTCCAGTGGGCTGGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 189  
QY 780 AACCAAGAGCTCTCAGATGCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 839  
Db 188 AACCAAGAGCTCTCAGATGCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 129  
QY 840 CAAGAGATTCAGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 899  
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Db 68 CCAGGACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 38

RESULT 6  
LOCUS AY401608 642 bp DNA linear GSS 15-DEC-2003  
DEFINITION Pan troglodytes GPR35 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION AY401608  
VERSION AY401608.1 GI:39757597  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
AUTHORS 1 (bases 1 to 642)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 642)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
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/db\_xref="taxon:9598"  
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Best Local Similarity 93.3%; Pred. No. 9.2e-119;  
Matches 599; Conservative 0; Mismatches 43; Indels 0; Gaps 0;  
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Db 1 ATGAATGACCATCAACATANTTGTGGCTCCAGTGANNTGCCCCCAACGATCAAG 60  
QY 61 CTGGGCTTCTAGCCCTACTTTGGGCGTCTGTGTGGTGTAGGCTGTGTCTCAACAGCCTG 120  
Db 61 CTCGNNNNNNCGCTACTTTGGGCGTCTGTGTGGTGTGGGCTGTCTCTCAACAGCCTG 120  
QY 121 GGGCTCTGGGTCTTCTGTGCGCATGACAGTGGAGCGAGACCGCGCATCTACATGACC 180  
Db 121 GGGCTCTGGGTCTTCTGTGCGCATGACAGTGGAGCGAGACCGCGCATGACCGC 180  
QY 181 AACCTGGGCGGTGGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
Db 181 AACCTGGGCGGTGGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
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Db 241 CGAGACACTCAGACACCGCGCTGTGCGCAGCTCTCCAGGGCATCTACCTGACCAACAGG 300  
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Db 361 CCGCTGCGTGGCGCGGCTGGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCTC 420  
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LOCUS CO923163 778 bp mRNA linear EST 16-AUG-2004  
DEFINITION AGENCOURT 30488658 NIH MGC 145 Homo sapiens cdna clone  
IMAGE:7211810 5', mRNA sequence.  
ACCESSION CO923163  
VERSION CO923163.1 GI:51275314  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens











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QY	624	GGCAGAGGCCACCGCAAGGCTAAACGCACTGCTGGGCCAACCTCTCTGCTGTGTGTGT	683
Db	792	GGCAGAGGCCACCCAAAGGCGCACCCACACATGCTGGGCCCACTTGGCTGTGTGTGT	851
QY	684	CTGCTTCTGCGCCCTGCAGCTGGGGGTGACAGTGGCGCTCGCAGTGGGCTGGAAGCGCTG	743
Db	852	CTGCTTCTGCGCCCTGTCATGTGTGCTGCTGACCGTGCAGGTCTCCCTGAACCTCAATACCTG	911
QY	744	TGCGCTCTCTGGAGACGATCCGTCGCGCCCTGTACATACCAAGCAAGCTTCTCAGATGCCAA	803
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DEFINITION		Mus musculus 12 days embryo embryonic body between diaphragm region	
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		product:G protein-coupled receptor 35, full insert sequence.	
ACCESSION	AK034870		
VERSION	AK034870.1	GI:26330261	
KEYWORDS		HTC; CAP trapper.	
SOURCE		Mus musculus (house mouse)	
ORGANISM		Mus musculus	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE			
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QY 30 CAGCGACCTCACCTGGCCCCCAGCGATCAAGCTTCTACGCTCTACTTGGGGTGCT 89  
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QY 924 CGCCTA 929  
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RESULT 12

AK089198

LOCUS

DEFINITION Mus musculus NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone: F630036B21 product: g protein-coupled receptor 35, full insert sequence.

ACCESSION AK089198

VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AK089198.1 GI:26105132

HTC; CAP trapper.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

99279253

10349636

REFERENCE

AUTHORS

1 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

11042159

REFERENCE

AUTHORS

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,

Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,

Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,

Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,

Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,

Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,

Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

20530913

11076861

REFERENCE

AUTHORS

4 The RIKEN Genome Exploration Research Group Phase II Team and the

FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

5 The FANTOM Consortium and the RIKEN Genome Exploration Research

Group Phase I &amp; II Team.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 4254)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,

Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,

Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,

Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T.,

Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,

Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,

Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,

Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,

Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,

Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,

Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of

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Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.jp,

URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,

Fax: 81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics

Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome

Trust/MRC building Addenbrookes Hospital Cambridge) whose

assistance we gratefully acknowledge.  
URL: <http://genome.gsc.riken.jp/>  
URL: <http://fantom.gsc.riken.jp/>  
Location/Qualifiers

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/note="G protein-coupled receptor 35 (MGI:1929509,  
GB|NM\_022320, evidence: BLASTN, 99%, match=2495)  
putative"

ORIGIN

Query Match 57.9%; Score 538.2; DB 3; Length 4254;  
Best Local Similarity 77.6%; Pred. No. 4.2e-107;  
Matches 704; Conservative 0; Mismatches 193; Indels 10; Gaps 4;  
QY 30 CAGCGACCTCACCTGCGCCCGAGCGATCAAGCTGGGCTTCTACGCTACTTGGGGCTCCT 89  
DB 448 CAGCACCCTCAGTGGCTGCTTCGGTCAACAACCTTCTTCATCATCTACTCAGCCTTGT 507  
QY 90 GCTGTGTAGCCCTGCTCTCAACAGCTGGCGTCTGGGTGTTCTGTGCGCATGCA 149  
DB 508 GCTGTGTGGGCTGCTCTCAACAGCTGGCATCTGGGTATTCTGTATCGCATGCA 567  
QY 150 GCAGTGGACGGAGACCGCGATCTACATGACCAACTGGCGGTGGCGGACCTTGTCTGT 209  
DB 568 CCAGTGGACAGAGACCGCATCTATATGACCAACCTGGCTGTGGCGGACCTTGTCTGT 627  
QY 210 GTGACCTTGGCTTGGCTGCTGCTCACTCCCTGGAGACA---CCTCAGACAGCCGCTGTG 266  
DB 628 GTGCTCTTGGCATTTGTGCTGTACTCTCCCTGAAATATATGTTCTTCAGACACACCGCTGTG 687  
QY 267 CCAGCTCTCCAGGGCATCTACTGACCAAGGTACATGACATCAGCTGCTGCACGGC 326  
DB 688 CCAGCTCTCAGGGCATCTACTGCGCAACAGATACATGACATAGCCTGGTGGTCACTGC 747  
QY 327 CATCCCGTGGACCGCTATGTGGCGGTGGCGCACCCGCTGCGTGGCGCGGCTCGGCTC 386  
DB 748 CATTGCTGTGACCGCTATGTGGCAGTGGCGCATCCCGTGGTGGTGGTGGTGGTGGT 807  
QY 387 CCCAGGACAGCTGCGGCGGTGTGGCGGTCTCTGGGTGTGGTGTATCGGCTCCCTGTGT 446  
DB 808 CCGGACAGGCTGACGAGTGTGTGGCGCTTTTGGGTGTATGTTGGTCACTCCCTGTGT 867  
QY 447 GCGTCTGCTGCTGCGGATTCAGAGGGCGGCTTCTGCTTCAGAGGAC---ACCGGCA 503  
DB 868 AGTGGCTGCGGCTGCGGATTCAGAGGGCGGCTTCTGCTTCAGAGGACAAACCGCGG 927  
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DB 928 CAATTTCAAGCACCCTGCTTCTCACTGCTGGGATTTCTACCTGCGCTGGGCTGGTGGT 987  
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DB 988 CTTCTGCTCTTTGACGAGTGTGACTGTGCTATCGAGAGGGCGAGCGCTGATGTGGGCA 1047  
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DB 1108 CTGCTTCTGCGCTTGTGATGTGGTCTGACCGTGGAGGTCTCCCTGAACTCAATACCTG 1167  
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QY 863 CACTGCGCGTGGCTCCCGTGTAAAGGCCCAAAAGCCAGGACTCTCTGTGGGTGACCC 922  
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QY 923 TCGCCCTA 929  
DB 1345 TCACCTA 1351

RESULT 13

CN835586  
LOCUS  
DEFINITION  
AGENCOURT\_15669742 NIH\_MGC\_145 Homo sapiens cDNA clone  
IMAGE:7001933 5', mRNA sequence.  
ACCESSION  
CN835586  
VERSION  
CN835586.1 GI:47941241  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 783)  
AUTHORS  
NIH-MGC <http://mgc.nci.nih.gov/>  
TITLE  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL  
Unpublished (1999)  
COMMENT  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: GPCR Consortium  
cDNA Library Preparation: GPCR Consortium  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: IRB13 row: a column: 03  
High quality sequence stop: 482.  
Location/Qualifiers

FEATURES

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varies by clone; ORFs were PCR-amplified and cloned into  
pcDNA3.1 by the GPCR Consortium. Cloning sites vary by  
clone and include the following: 5'-EcoRV-XmaI/XhoI-3',  
5'-EcoRV-XmiI/NotI-3', EcoRV (TA cloned, non-directional).  
For information about which gene each clones represents,  
please visit our anonymous ftp site at  
[ftp://image.llnl.gov/image/rearrayed\\_plates/IRB1.preSV.dat](ftp://image.llnl.gov/image/rearrayed_plates/IRB1.preSV.dat)  
a Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 57.1%; Score 531.2; DB 7; Length 783;  
Best Local Similarity 94.2%; Pred. No. 1.2e-105;  
Matches 585; Conservative 0; Mismatches 29; Indels 7; Gaps 3;  
QY 1 ATGAATGCACTTACCAACACCTGTGGCTCCAGGACCTCACCTGGCCCCCAGCGATCAAG 60  
DB 9 ATGAATGCACTTACCAACACCTGTGGCTCCAGGACCTCACCTGGCCCCCAGCGATCAAG 68

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Db 129 GCGCTCTGGGTTCTGCTGCGGCTATGACAGCTGCGAGAGAGAGAGAGAGAGAGAGAG 188
QY 181 AACCTGGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Db 189 AACCTGGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 248
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QY 301 TACATGAGCATCAGCTGCTACGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 360
Db 309 TACATGAGCATCAGCTGCTACGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 368
QY 361 CCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 420
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QY 481 TTCTGCTTTCAGGAGCAGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 538
Db 489 TTCTGCTTTCAGGAGCAGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 548
QY 539 TCTACTGCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCG 593
Db 549 TCTACTGCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCG 608
QY 594 GCGCCAGAGGCGCCACCCACCGA 614
Db 609 CTGGCCCGAGGAGGCCACCCCA 629
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RESULT 14
CO923285/c
LOCUS CO923285 717 bp mRNA linear EST 16-AUG-2004
DEFINITION AGENCOURT_30698418 NIH_MGC_145 Homo sapiens cDNA clone
IMAGE:7211810 3', mRNA sequence.
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CO923285
CO923285.1 GI:51275562
EST.
Homo sapiens (human)
Homo sapiens
Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 717)
NIH-MGC http://mgi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs-remail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Prepared by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Cloned through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
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## FEATURES

Location/Qualifiers

## source

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/lab_host="DH10B"
/clone_lib="NIH_MGC_145"
/vector="pCDNA3.1; Site 1: varies by clone; Site 2:
varies by clone; ORFs were PCR-amplified and cloned into
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
clone and include the following: 5'-EcoRV-XmiI/XhoI-3',
5'-EcoRV-XmiI/NotI-3', EcoRV (TA cloned, non-directional).
For information about which gene each clone represents,
please visit our anonymous ftp site at
ftp://image.llnl.gov/image/rearrayed_plates/IRB1.preSV.dat
a Note: this is a NIH_MGC Library."
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## ORIGIN

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Query Match 55.5%; Score 516.6; DB 7; Length 717;
Best Local Similarity 96.4%; Pred. No. 1.9e-102;
Matches 539; Conservative 0; Mismatches 19; Indels 1; Gaps 1;
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Db 596 CCCCCGGTGGCGTCCCCCAGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 538
QY 432 CATCGGCTCCCTGGTGGCTGCGTGGCTGCGTGGGATTCAGAGGGGGGCTTCTGCTTCAG 491
Db 537 CATCGGCTCCCGGTTGGCTGCGTGGCTGCGTGGGATTCAGAGGGGGGCTTCTGCTTCAG 478
QY 492 GAGCACCAGGACAAATTTCACTCCATCGGTTCCCGCTGCTGGGATTCCTACTGCCCCCT 551
Db 477 GAGCACCAGGACAAATTTCACTCCATCGGTTCCCGCTGCTGGGATTCCTACTGCCCCCT 418
QY 552 GCGCGTGGTGGTCTTCTGCTCCCTGAAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 611
Db 417 GCGCGTGGTGGTCTTCTGCTCCCTGAAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 358
QY 612 CGACGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 671
Db 357 CGACGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 298
QY 672 GGTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 731
Db 297 GGTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 238
QY 732 CTGGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 791
Db 237 CTGGAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 178
QY 792 CTCAGATGCCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 851
Db 177 CTCAGATGCCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 118
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QY 912 GTGCGTGACCCCTCGGCTAA 930
Db 57 GTGCGTGACCCCTCGGCTAA 39
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## RESULT 15

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CO9232122/c
LOCUS CO9232122 1019 bp mRNA linear EST 02-JUN-2004
DEFINITION AGENCOURT_15864152 NIH_MGC_145 Homo sapiens cDNA clone
IMAGE:7001931 3', mRNA sequence.
CO9232122
CO9232122.1 GI:47935875
EST.
Homo sapiens (human)
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 11:33:12 ; Search time 2849 Seconds  
(without alignments)  
2001.776 Million cell updates/sec

Title: US-10-083-168-84  
Perfect score: 930  
Sequence: 1 atgaatggcaactcaacac.....tgtcggtgacctgcctaa 930

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5695437 seqs, 3066160638 residues

Total number of hits satisfying chosen parameters: 11390874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	930	100.0	930	14	US-10-083-168-84
2	925.2	99.5	930	14	Sequence 84, Appl
3	925.2	99.5	930	15	Sequence 15, Appl
4	925.2	99.5	930	15	Sequence 491, App
5	920.4	99.0	1875	9	Sequence 6, Appl
6	920.4	99.0	1875	9	Sequence 21, Appl
7	920.4	99.0	1875	15	Sequence 350, App
8	916.8	99.0	49136	9	Sequence 1, Appli
9	900	96.8	24477	19	Sequence 17827, A
10	200.6	21.6	201	15	Sequence 636, App
11	200.6	21.6	201	19	Sequence 61537, A
					Sequence 61547, A

12	200.6	21.6	201	19	US-10-741-600-61549	Sequence 61549, A
13	200.6	21.6	201	19	US-10-741-600-61551	Sequence 61551, A
14	200.6	21.6	201	19	US-10-741-600-61552	Sequence 61552, A
15	200.6	21.6	201	19	US-10-741-600-61567	Sequence 61567, A
16	200.6	21.6	201	19	US-10-741-600-61568	Sequence 61568, A
17	197.4	21.2	201	19	US-10-741-600-61525	Sequence 61525, A
18	197.4	21.2	201	19	US-10-741-600-61532	Sequence 61532, A
19	197.4	21.2	201	19	US-10-741-600-61535	Sequence 61535, A
20	195.8	21.1	201	19	US-10-741-600-61565	Sequence 61565, A
21	172.6	18.6	201	19	US-10-741-600-61546	Sequence 61546, A
22	150.6	16.2	201	19	US-10-741-600-61524	Sequence 61524, A
23	141.8	15.2	1854	10	US-09-866-050A-596	Sequence 596, App
24	141.8	15.2	1854	14	US-10-152-661-596	Sequence 596, App
25	111.6	12.0	1098	15	US-10-251-385-225	Sequence 225, App
26	111.2	12.0	1089	15	US-10-251-385-3	Sequence 3, Appli
27	111.2	12.0	1089	15	US-10-267-811-1	Sequence 1, Appli
28	111.2	12.0	1365	15	US-10-101-510-17	Sequence 17, Appli
29	111.2	12.0	1365	17	US-10-305-720-1429	Sequence 1429, App
30	111.2	12.0	1365	18	US-10-283-975A-113	Sequence 113, App
31	111.2	12.0	2693	10	US-09-850-948-1	Sequence 1, Appli
32	111.2	12.0	2693	15	US-10-273-575-1	Sequence 1, Appli
33	111.2	12.0	2696	15	US-10-225-567A-272	Sequence 272, App
34	111.2	12.0	2980	15	US-10-101-510-456	Sequence 456, App
35	110.4	11.9	1617	14	US-10-167-192-2	Sequence 2, Appli
36	110.4	11.9	1617	17	US-10-400-991-5	Sequence 5, Appli
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39	110	11.8	1098	15	US-10-273-575-5	Sequence 5, Appli
40	110	11.8	1098	15	US-10-225-567A-282	Sequence 282, App
41	110	11.8	1434	16	US-10-029-386-25332	Sequence 25332, A
42	110	11.8	1697	14	US-10-109-533A-1	Sequence 1, Appli
43	110	11.8	1697	15	US-10-288-222A-11	Sequence 11, Appli
44	109.6	11.8	1089	15	US-10-251-385-165	Sequence 165, App
45	107.6	11.6	1254	18	US-10-484-788-13	Sequence 13, Appli

ALIGNMENTS

RESULT 1

US-10-083-168-84  
; Sequence 84, Application US/10083168  
; Publication No. US20030023069A1  
; GENERAL INFORMATION:  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Maciejewski-Lenior, Dominique  
; APPLICANT: Leonard, James N.  
; APPLICANT: Ortuno, Daniel  
; APPLICANT: Lin, I-Lin  
; TITLE OF INVENTION: Endogenous And No. US20030023069A1-Endogenous, Constitutively Acr  
; TITLE OF INVENTION: Receptors  
; FILE REFERENCE: AREN-0320  
; CURRENT APPLICATION NUMBER: US/10/083,168  
; CURRENT FILING DATE: 2002-02-26  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 84  
; LENGTH: 930  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: No.. US20030023069A1el Sequence  
US-10-083-168-84

Query Match 100.0%; Score 930; DB 14; Length 930;  
Best Local Similarity 100.0%; Pred. No. 2e-225;  
Matches 930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGGCACTTACACACCTGTGGCTCCAGCGACCTCACCTGGCCCCCAGGATCAAG 60

DB 1 ATGATGGCACTTACACACCTGTGGCTCCAGCGACCTCACCTGGCCCCCAGGATCAAG 60



[illegible]

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; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Endogenous And No. US20030023069A1-Endogenous, Constitutively Act
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0320
; CURRENT APPLICATION NUMBER: US/10/083,168
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 930
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-083-168-15

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RESULT 2  
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; Sequence 15, Application US/10083168  
; Publication No. US20030023069A1  
; GENERAL INFORMATION:  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Chalmers, Derek T.  
; APPLICANT: Behan, Dominic P.  
; APPLICANT: Maciejewski-Lenior, Dom  
; APPLICANT: Leonard, James N.  
; APPLICANT: Ortuno, Daniel



QY 841 AAGGAGTTCCAGGAGCGTCTGCACTGGCGGTGGCTCCCGTGTCTAAGGCCCAAAAAAGC 900  
DB 841 AAGGAGTTCCAGGAGCGTCTGCACTGGCGGTGGCTCCCGTGTCTAAGGCCCAAAAAAGC 900  
QY 901 CAGGACTCTCTGTGGTGCACCTCGCCTAA 930  
DB 901 CAGGACTCTCTGTGGTGCACCTCGCCTAA 930

## RESULT 3

US-10-225-567A-491  
; Sequence 491, Application US/10225567A  
; Publication No. US20030113798A1  
; GENERAL INFORMATION:  
; APPLICANT: LifeSpan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burmer, Glenna C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/257,144  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 491  
; LENGTH: 930  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-225-567A-491

Query Match 99.5%; Score 925.2; DB 15; Length 930;  
Best Local Similarity 99.7%; Pred. No. 3.2e-224;  
Matches 927; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 361 CGGCTGTGCTGGCGGCTGGGCTCCCGCAGGAGGCTGGCGCGTGTGGCGGTCTCTC 420  
QY 421 TGGGTGTGGTCTAGCGGTCTCTGTGGTCTGGCTCTGGGTCTGGGTCTGGGTCTGG 480  
DB 421 TGGGTGTGGTCTAGCGGTCTCTGTGGTCTGGCTCTGGGTCTGGGTCTGGGTCTGG 480  
QY 481 TTCTGTCTCAGGAGCACCGGCAAAATTCATCTCCATCGGTTCCCGTCTGCTGGATTC 540  
DB 481 TTCTGTCTCAGGAGCACCGGCAAAATTCATCTCCATCGGTTCCCGTCTGCTGGATTC 540

QY 541 TACCTGCCCTTGGCGGTGGTCTTCTGTCTCCCTGAAGGTGGTGAATGCTGCCCTGGCCAG 600  
DB 541 TACCTGCCCTTGGCGGTGGTCTTCTGTCTCCCTGAAGGTGGTGAATGCTGCCCTGGCCAG 600  
QY 601 AGGCACCCACCGAGCTGGGGCAGCAGAGGCCACCCGCAAGGCTAAACGATGTCTGG 660  
DB 601 AGGCACCCACCGAGCTGGGGCAGCAGAGGCCACCCGCAAGGCTAAACGATGTCTGG 660  
QY 661 GCCAACCTCTCTGTGGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 720  
DB 661 GCCAACCTCTCTGTGGTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 720  
QY 721 CTGCGAGTGGGCTGGAACGCTGTGCCCTCTGTGGAGAGATCCGCTCGCGCCCTGTACATA 780  
DB 721 CTGCGAGTGGGCTGGAACGCTGTGCCCTCTGTGGAGAGATCCGCTCGCGCCCTGTACATA 780  
QY 781 ACCAGCAAGCTCTCAGATGCCAACTGTGCTCTGGACGCCATCTGCTACTACTATGCGC 840  
DB 781 ACCAGCAAGCTCTCAGATGCCAACTGTGCTCTGGACGCCATCTGCTACTACTATGCGC 840  
QY 841 AAGGAGTTCCAGGAGCGCTCTGCACTGGCGGTGGCTCCCGTGTCTAAGGCCCAAAAAAGC 900  
DB 841 AAGGAGTTCCAGGAGCGCTCTGCACTGGCGGTGGCTCCCGTGTCTAAGGCCCAAAAAAGC 900  
QY 901 CAGGACTCTCTGTGGTGCACCTCGCCTAA 930  
DB 901 CAGGACTCTCTGTGGTGCACCTCGCCTAA 930

## RESULT 4

US-10-696-639-6  
; Sequence 6, Application US/10696639  
; Publication No. US20050037439A1  
; GENERAL INFORMATION:  
; APPLICANT: Pharmacia Corporation  
; APPLICANT: Bourner, Maureen J.  
; TITLE OF INVENTION: DIFFERENTIALLY EXPRESSED GENES INVOLVED IN CANCER, THE SAME  
; FILE REFERENCE: 01040/1  
; CURRENT APPLICATION NUMBER: US/10/696,639  
; CURRENT FILING DATE: 2003-10-29  
; PRIOR APPLICATION NUMBER: 60/422,176  
; PRIOR FILING DATE: 2002-10-29  
; NUMBER OF SEQ ID NOS: 3114  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 6  
; LENGTH: 930  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-696-639-6

Query Match 99.5%; Score 925.2; DB 19; Length 930;  
Best Local Similarity 99.7%; Pred. No. 3.2e-224;  
Matches 927; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAATGGCACTACAAACCTGTGGCTCCAGCGACCTCACTGGCCCCCAGCGATCAAG 60  
DB 1 ATGAATGGCACTACAAACCTGTGGCTCCAGCGACCTCACTGGCCCCCAGCGATCAAG 60  
QY 61 CTGGGCTTCTAGCGTCTAGCGGTCTCTGTGGTCTAGGCTTCTCTCAACAGCTG 120  
DB 61 CTGGGCTTCTAGCGTCTAGCGGTCTCTGTGGTCTAGGCTTCTCTCAACAGCTG 120  
QY 121 CGGCTCTGGGTCTCTGTGCTGCGATGCGAGTGGAGCGGACCGCATCTACATGACC 180  
DB 121 CGGCTCTGGGTCTCTGTGCTGCGATGCGAGTGGAGCGGACCGCATCTACATGACC 180  
QY 181 AACCTGGCGGTGGCGGACCTCTGCTGTGCACTTGGCTTCTGGCTGCACTCCCTG 240  
DB 181 AACCTGGCGGTGGCGGACCTCTGCTGTGCACTTGGCTTCTGGCTGCACTCCCTG 240  
QY 241 CGAGACACTCAGACACCGCGCTGTGCCAGCTCTCCAGGGGATCTACTGACCAACAGG 300

[illegible]

## RESULT 5

US-09-768-877-21

; Sequence 21, Application US/09768877

; Patent No. US20020150896A1

**GENERAL INFORMATION:**

APPLICANT: POLONSKY, KENNETH S.

APPLICANT: HORIKAWA, YUKIO

APPLICANT: ODA, NAOHISA

APPLICANT: COX, NANCY J.

APPLICANT: SREENAN, SEAMUS

; APPLICANT: ZHOU, YUN-PING

APPLICANT: OTANI, KENICHI

APPLICANT: HANIS, CRAIG

; APPLICANT: BELL, GRAEME

; TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES

; FILE REFERENCE: ARCD:307

; CURRENT APPLICATION NUMBER: US/09/768,877

; CURRENT FILING DATE: 2001-01-23

; PRIOR APPLICATION NUMBER: 09/422,869

; PRIOR FILING DATE: 1999-10-21

; NUMBER OF SEQ ID NOS: 30

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; SOFTWARE: PatentIn Ver. 2.0
```

; SEQ ID NO 21

; LENGTH: 1875

; TYPE: DNA

; ORGANISM: Human

US-09-768-877-21

Query Match 99.0%; Score 920.4; DB 9; Length 1875;

Best Local Similarity 99.4%; Pred. No. 5.3e-223;

Matches	924	Conservative	0	Mismatches	6	Indels	0	Gaps	0
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QY	1	ATGAATGGC	ACTTACACAC	CTGTGGCT	CACGGAC	CTTCACT	TGGCCCCC	CAGCGAT	CAAG	60		
DB	576	ATGAATGGC	ACTTACACAC	CTGTGGCT	CACGGAC	CTTCACT	TGGCCCCC	CAGCGAT	CAAG	635		
QY	61	CTGGGCTT	CACGCTACT	TTTGGGCGT	CTCTGT	TGGTGT	TAGSCCT	TGCTCAAC	CAGCGCTG	120		
DB	636	CTGGGCTT	CACGCTACT	TTTGGGCGT	CTCTGT	TGGTGT	TAGSCCT	TGCTCAAC	CAGCGCTG	695		
QY	121	CGCCTCT	TGGGTGTT	CTGCT	CCGCAT	GCAGCAG	TGAGCGG	AGACCC	CGCATCTAT	CATGACC	180	
DB	696	CGCCTCT	TGGGTGTT	CTGCT	CCGCAT	GCAGCAG	TGAGCGG	AGACCC	CGCATCTAT	CATGACC	755	
QY	181	AACCTGG	CGGTGGC	CGACCT	CTGGCT	CTGTGC	ACCTTGGCCT	TGCTGTC	GTGCACTCCCTG	240		
DB	756	AACCTGG	CGGTGGC	CGACCT	CTGGCT	CTGTGC	ACCTTGGCCT	TGCTGTC	GTGCACTCCCTG	815		
QY	241	CGAGAC	CACTCAG	ACACG	CGCTGT	TGCACT	CTCCAC	GGGCATCT	ACCTGAC	CAACAGG	300	
DB	816	CGAGAC	CACTCAG	ACACG	CGCTGT	TGCACT	CTCCAC	GGGCATCT	ACCTGAC	CAACAGG	875	
QY	301	TACATG	AGCATCAG	CCCTG	TACGGCC	ATCG	CCGTGG	ACCGCTAT	TGCGCGT	CGGCAC	360	
DB	876	TACATG	AGCATCAG	CCCTG	TACGGCC	ATCG	CCGTGG	ACCGCTAT	TGCGCGT	CGGCAC	935	
QY	361	CCGCTG	CGTGCC	CGCGGCT	CGGTC	CCCA	GGCAGC	CTGGG	CCGTGTGGG	CGGTCCTC	420	
DB	936	CCGCTG	CGTGCC	CGCGGCT	CGGTC	CCCA	GGCAGC	CTGGG	CCGTGTGGG	CGGTCCTC	995	
QY	421	TGGGTG	CTGTG	TATCG	CGCTCC	TGCTG	CGCTCT	CTGGGG	ATTCAGG	AGGGCGGC	480	
DB	996	TGGGTG	CTGTG	TATCG	CGCTCC	TGCTG	CGCTCT	CTGGGG	ATTCAGG	AGGGCGGC	1055	
QY	481	TTCTGCT	TTCAGG	AGCAC	CCCG	GCACAA	TTTCAA	CTCCAT	TGCGGTTCC	CGCTGCTGGGATTC	540	
DB	1056	TTCTGCT	TTCAGG	AGCAC	CCCG	GCACAA	TTTCAA	CTCCAT	TGCGGTTCC	CGCTGCTGGGATTC	1115	
QY	541	TACCTG	CGCCTGG	CGGTGGT	GCTTCT	TGCTC	CTGAA	GGTGGT	GTGACTG	CGCTGGCCCGAC	600	
DB	1116	TACCTG	CGCCTGG	CGGTGGT	GCTTCT	TGCTC	CTGAA	GGTGGT	GTGACTG	CGCTGGCCCGAC	1175	
QY	601	AGGCCA	CCACCG	ACGTGGG	CGACG	AGSCC	ACC	CGCA	AGGCTAAA	CGCATGCTCTGG	660	
DB	1176	AGGCCA	CCACCG	ACGTGGG	CGACG	AGSCC	ACC	CGCA	AGGCTAAA	CGCATGCTCTGG	1235	
QY	661	GCCAACT	CTCTGT	GTGTT	CGTGGT	CTGTT	CTGTG	CCCTG	CACTG	CGGCGTGCAC	AGTGC	720
DB	1236	GCCAACT	CTCTGT	GTGTT	CGTGGT	CTGTT	CTGTG	CCCTG	CACTG	CGGCGTGCAC	AGTGC	1295
QY	721	CTCGAG	TGGGCTG	GAAC	CGCTG	TCCT	GTGAG	ACGAT	CCGTG	CGGCCCTGT	TACATA	780
DB	1296	CTCGAG	TGGGCTG	GAAC	CGCTG	TCCT	GTGAG	ACGAT	CCGTG	CGGCCCTGT	TACATA	1355
QY	781	ACACG	AGCTCT	CAGAT	GGCA	ACTG	CTGCT	GTGAC	CGCAT	CTCTACT	ACTATG	840
DB	1356	ACACG	AGCTCT	CAGAT	GGCA	ACTG	CTGCT	GTGAC	CGCAT	CTCTACT	ACTATG	1415
QY	841	AAGGAG	TTCCAG	GAGG	CGTGT	GCAC	TG	CGGTG	GCTCC	CGTGTAA	AGGCCAC	900
DB	1416	AAGGAG	TTCCAG	GAGG	CGTGT	GCAC	TG	CGGTG	GCTCC	CGTGTAA	AGGCCAC	1475
QY	901	CAGG	ACTCT	TGTGG	GTGA	CCCT	CGCCT	ATA	930			
DB	1476	CAGG	ACTCT	TGTGG	GTGA	CCCT	CGCCT	ATA	1505			

## RESULT 6

US-10-157-031-350

```
; Sequence 350, Application US/10157031
; Publication No. US20030108890A1
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobashev, A. V.
; APPLICANT: Krukovskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157,031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 350
; LENGTH: 1875
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-157-031-350

Query Match      99.0%; Score 920.4; DB 15; Length 1875;
Best Local Similarity 99.4%; Pred. No. 5.3e-223;
Matches 924; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 ATGAATGGCACTACAAACACCTGTGGCTCCAGGACCTCAGCTGGCCCCCAGCGATCAAG 60
DB      576 ATGAATGGCACTACAAACACCTGTGGCTCCAGGACCTCAGCTGGCCCCCAGCGATCAAG 635

QY      61 CTGGGCTTCTACGCTACTTGGGGCTCTGCTGGTGTAGGCTGCTGCTCAACAGCCTG 120
DB      636 CTGGGCTTCTACGCTACTTGGGGCTCTGCTGGTGTAGGCTGCTGCTCAACAGCCTG 695

QY      121 GCGCTCTGGGTGTTCTGTGCGGATAGCAGAGTGGAGCGGACCCGATCTACATGACC 180
DB      696 GCGCTCTGGGTGTTCTGTGCGGATAGCAGAGTGGAGCGGACCCGATCTACATGACC 755

QY      181 AACCTGGCGGTGGCGAGCTCTGCTGCTGTGACCTTGGCTTGGCTTGGCTGCTGCTGCTG 240
DB      756 AACCTGGCGGTGGCGAGCTCTGCTGCTGTGACCTTGGCTTGGCTTGGCTGCTGCTGCTG 815

QY      241 CGAGACACTCAGACACCGCGTGTGCGAGCTCTCCAGGGGATCTACTGACCAACAGG 300
DB      816 CGAGACACTCAGACACCGCGTGTGCGAGCTCTCCAGGGGATCTACTGACCAACAGG 875

QY      301 TACATGACATCAGCTGTTCAAGCCCATTCGCGTGGACCGCTATGTGGCGGTGCGGCAC 360
DB      876 TACATGACATCAGCTGTTCAAGCCCATTCGCGTGGACCGCTATGTGGCGGTGCGGCAC 935

QY      361 CGCTGCGTGGCGGGGCTGGGTCCCGCAGGAGGCTGCGGCGGTGTGGCGGTGCTCTC 420
DB      936 CGCTGCGTGGCGGGGCTGGGTCCCGCAGGAGGCTGCGGCGGTGTGGCGGTGCTCTC 995

QY      421 TGGGTGCTGCTCATCGGCTCCCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB      996 TGGGTGCTGCTCATCGGCTCCCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1055

QY      481 TTCTGCTTTCAAGAGCACCGGCAAAATTTCAACTCCATGCGGTTCCCGCTGTGGGATTC 540
DB      1056 TTCTGCTTTCAAGAGCACCGGCAAAATTTCAACTCCATGCGGTTCCCGCTGTGGGATTC 1115

QY      541 TACTTGCCCTTGGCGGCTGGTGTCTTCTGCTCCCTGAAAGGTGGTGAATGCTGCTGCGCCAG 600
DB      1116 TACTTGCCCTTGGCGGCTGGTGTCTTCTGCTCCCTGAAAGGTGGTGAATGCTGCTGCGCCAG 1175

QY      601 AGGCCACCCACGAGTGGGCGAGGAGGCCACCCGACAGGCTAAACGATGCTCTGG 660
DB      1176 AGGCCACCCACGAGTGGGCGAGGAGGCCACCCGACAGGCTAAACGATGCTCTGG 1235

QY      661 GCCAACCTCTCTGGTGTCTGCTGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB      1236 GCCAACCTCTCTGGTGTCTGCTGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1295

QY      721 CTCGCAAGTGGGCTGGAACCGCTGTGCCCTCTCTCTGAGAGAGATCCGCTGCGGCCCTGTACATA 780
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DB      1296 CTCGCAAGTGGGCTGGAACCGCTGTGCCCTCTCTGAGAGAGATCCGCTGCGGCCCTGTACATA 1355
QY      781 ACCAGCAAGCTCTCAGATGCCAACTGTGCTTGGAGCGCATCTGCTACTTACTTACATGGCC 840
DB      1356 ACCAGCAAGCTCTCAGATGCCAACTGTGCTTGGAGCGCATCTGCTACTTACTTACATGGCC 1415
QY      841 AAGGAGTTCAGGAGGCGTCTGCACTGGCGTGGCTTCCCGTGTAAAGGCCACAAAGC 900
DB      1416 AAGGAGTTCAGGAGGCGTCTGCACTGGCGTGGCTTCCCGTGTAAAGGCCACAAAGC 1475
QY      901 CAGGACTCTCTGTGCGTGACCTCGCCTAA 930
DB      1476 CAGGACTCTCTGTGCGTGACCTCGCCTAA 1505

RESULT 7
US-09-768-877-1
; Sequence 1, Application US/09768877
; Patent No. US20020150896A1
; GENERAL INFORMATION:
; APPLICANT: POLONSKY, KENNETH S.
; APPLICANT: HORIKAWA, YUKIO
; APPLICANT: ODA, NAOHISA
; APPLICANT: COX, NANCY J.
; APPLICANT: SREENAN, SEAMUS
; APPLICANT: ZHOU, YUN-PING
; APPLICANT: OTANI, KENICHI
; APPLICANT: HANIS, CRAIG L.
; APPLICANT: BELL, GRAEME I.
; TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES
; FILE REFERENCE: ARCD:307
; CURRENT APPLICATION NUMBER: US/09/768,877
; CURRENT FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 09/422,869
; PRIOR FILING DATE: 1999-10-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 1
; LENGTH: 49136
; TYPE: DNA
; ORGANISM: Human
US-09-768-877-1

Query Match      99.0%; Score 920.4; DB 9; Length 49136;
Best Local Similarity 99.4%; Pred. No. 5.5e-223;
Matches 924; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 ATGAATGGCACTACAAACACCTGTGGCTCCAGGACCTCAGCTGGCCCCCAGCGATCAAG 60
DB      43645 ATGAATGGCACTACAAACACCTGTGGCTCCAGGACCTCAGCTGGCCCCCAGCGATCAAG 43704

QY      61 CTGGGCTTCTACGCTACTTGGGGCTCTGCTGGTGTAGGCTGCTGCTCAACAGCCTG 120
DB      43705 CTGGGCTTCTACGCTACTTGGGGCTCTGCTGGTGTAGGCTGCTGCTCAACAGCCTG 43764

QY      121 GCGCTCTGGGTGTTCTGTGCGCGATGAGCAGTGGAGCGAGACCCGATCTTACATGACC 180
DB      43765 GCGCTCTGGGTGTTCTGTGCGCGATGAGCAGTGGAGCGAGACCCGATCTTACATGACC 43824

QY      181 AACCTGGCGGTGGCGAGCTCTGCTGCTGTGTGACCTTGGCTTGGCTTGGCTGCTGCTGCTG 240
DB      43825 AACCTGGCGGTGGCGAGCTCTGCTGCTGTGTGACCTTGGCTTGGCTTGGCTGCTGCTGCTG 43884

QY      241 CGAGACACTCAGACACCGCGCTGTGCCAGCTCTCCAGGGGATCTACTGACCAACAGG 300
DB      43885 CGAGACACTCAGACACCGCGCTGTGCCAGCTCTCCAGGGGATCTACTGACCAACAGG 43944

QY      301 TACATGACATCAGCTGTTCAAGCCCATTCGCGTGGACCGCTATGTGGCGGTGCGGCAC 360
DB      43945 TACATGACATCAGCTGTTCAAGCCCATTCGCGTGGACCGCTATGTGGCGGTGCGGCAC 44004

QY      361 CGCTGCGTGGCGGGCTGCGGTCTCCCGCAGGAGGCTGCGGCGGTGTGCGCGGTCTCTC 420
```



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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1912)
; OTHER INFORMATION: a, t, c, g, other or unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1928)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-101-510-636

Query Match          96.8%; Score 900; DB 15; Length 1989;
Best Local Similarity 99.2%; Pred. No. 7.6e-218;
Matches 925; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

QY 1 ATGAATGGCACTTACAACACCTGTGGCTCCAGGACCTCACTGGCCCCCAGCGATCAAG 60
DB 214 ATGAATGGCACTTACAACACCTGTGGCTCCAGGACCTCACTGGCCCCCAGCGATCAAG 273
QY 61 CTGGGCTTCTAGCCTTACTTGGGGCTCTGCTGGTGTAGGCTGTCTCAACAGCTG 120
DB 274 CTGGGCTTCTAGCCTTACTTGGGGCTCTGCTGGTGTAGGCTGTCTCAACAGCTG 333
QY 121 GCGCTCTGGGTGTTCTGCTGCCGATGACAGAGTGGAGGAGACCGGATCTACATGACC 180
DB 334 GCGCTCTGGGTGTTCTGCTGCCGATGACAGAGTGGAGGAGACCGGATCTACATGACC 393
QY 181 AACCTGGGGTGGCGGACCTCTGCTGTGTGACCTTGGCCCTTGTGTGCACTCCCTG 240
DB 394 AACCTGGGGTGGCGGACCTCTGCTGTGTGACCTTGGCCCTTGTGTGCACTCCCTG 453
QY 241 CGAGACA-CCTGAGACAGCCGCTGTGCCAGCTCTTCCAGGGGATCTACCTGACCAACAG 299
DB 454 CGAGACAGCTTCAAGACAGCCGCTGTGCCAGCTCTTCCAGGGGATCTACCTGACCAACAG 513
QY 300 GTACATGAGCATCAGCTGTTCACGGCCATCCGCTGGACCCGCTATGTGGCCGTGGCA 359
DB 514 GTACATGAGCATCAGCTGTTCACGGCCATCCGCTGGACCCGCTATGTGGCCGTGGCA 573
QY 360 CCGCTGTGCTGCCGCGGCT-GCGGTCCCGCAGGAGGCTCGGCGCTGTGCGGGTCC 418
DB 574 CCGCTGTGCTGCCGCGGCTCGGCGCTCCCGCAGGAGGCTCGGCGCTGTGCGGGTCC 633
QY 419 TCTGGGTGCTGTGATTCGGCTCCCTGGTGGCTCGCTGGCTCTGGGGAATCAGAGGGG 478
DB 634 TCTGGGTGCTGTGATTCGGCTCCCTGGTGGCTCGCTGGCTCTGGGGAATCAGAGGGG 693
QY 479 GCTTCTGCTTCAAGGAGCACCGGCAATTTCAACTCCATCGGTTCCGCTGCTGGGAT 538
DB 694 GCTTCTGCTTCAAGGAGCACCGGCAATTTCAACTCCATCGGTTCCGCTGCTGGGAT 753
QY 539 TCTACTGCTTCCGCTGGCTGGTGTCTTCTGCTCCCTGAAGGTGGTGAATGCTGGCC 598
DB 754 TCTACTGCTTCCGCTGGCTGGTGTCTTCTGCTCCCTGAAGGTGGTGAATGCTGGCC 813
QY 599 AGAGGCCACCCAGCAGTGGGGAGGAGAGGCCACCGCAAGGCTAAACGATGGTCT 658
DB 814 AGAGGCCACCCAGCAGTGGGGAGGAGAGGCCACCGCAAGGCTGGCCGATGGTCT 873
QY 659 GGGCCAACTCTGTGTGCTGGTGTCTTCTGCTCCCTGACGCTGGGCTGACAGTGC 718
DB 874 GGGCCAACTCTGTGTGCTGGTGTCTTCTGCTCCCTGACGCTGGGCTGACAGTGC 933
QY 719 GCTCGCAGTGGCTGGAACGCTGTGCCCTCTCGAGACGATCCGTCGCGCCCTGTACA 778
DB 934 GCTCGCAGTGGCTGGAACGCTGTGCCCTCTCGAGACGATCCGTCGCGCCCTGTACA 993
QY 779 TAACAGCAAGCTCTCAGATGCCAATCTGTGCTGGAGCGCCATCTGTCTACTACTAGG 838
DB 994 TAACAGCAAGCTCTCAGATGCCAATCTGTGCTGGAGCGCCATCTGTCTACTACTAGG 1053
QY 839 CCAAGAGTTTCAAGAGGCTGTGCACTGGCCGCTGCCCTCCGCTGCTAAGGCCACAAA 898
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DB 1054 CCAAGGAGTTCAGGAGGCTGTGCACTGGCGCTGGCTCCCGTGAAGGCCACAAAA 1113
QY 899 GCCAGGACTCTCTGTGCGTGAGCCCTCGGCTAA 930
DB 1114 GCCAGGACTCTCTGTGCGTGAGCCCTCGGCTAA 1145

RESULT 10
US-10-741-600-61537
; Sequence 61537, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61537
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-61537

Query Match          21.6%; Score 200.6; DB 19; Length 201;
Best Local Similarity 99.5%; Pred. No. 4.7e-41;
Matches 200; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 223 TTGCTGCTGCACTCCCTGGGAGACACCTCAGACACGCGCTGTGCAGCTCTCCAGGGC 282
DB 1 TTGCTGCTGCACTCCCTGGGAGACACCTCAGACACGCGCTGTGCAGCTCTCCAGGGC 60
QY 283 ATCTACCTGACCAACAGGTACATGAGCATCAGCCTGTGTCAGCCATCGCCGTGACCGC 342
DB 61 ATCTACCTGACCAACAGGTACATGAGCATCAGCCTGTGTCAGCCATCGCCGTGACCGC 120
QY 343 TATGCGCGCTGGCGACCCGCTGCTGCGCGGCTGCGGTCCCGAGGAGGCTGCG 402
DB 121 TATGCGCGCTGGCGACCCGCTGCTGCGCGGCTGCGGTCCCGAGGAGGCTGCG 180
QY 403 GCGGTGTGCGGCTCTCTGG 423
DB 181 GCGGTGTGCGGCTCTCTGG 201

RESULT 11
US-10-741-600-61547
; Sequence 61547, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61547
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-61547

Query Match          21.6%; Score 200.6; DB 19; Length 201;
Best Local Similarity 99.5%; Pred. No. 4.7e-41;
Matches 200; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 23 GTGGCTCCAGGACCTCACTGGCCCCCAGCGATCAAGCTGGCTTCTACGCTACTTGG 82
DB 1 GTGGCTCCAGGACCTCACTGGCCCCCAGCGATCAAGCTGGGCTTCTACGCTACTTGG 60
```

```
QY      83 GGGTCTGTGCTAGGCTGTGCTCAACAGCTGGCGCTCTGGGTGTTCTGCTGCC 142
      |||
Db      61 GGGTCTGTGCTAGGCTGTGCTCAACAGCTGGCGCTCTGGGTGTTCTGCTGCC 120
      |||
QY     143 GCATCAGCAGTGGAGCGAGACCCGCTATCATGACCAACTGGCGGTGGCCGACCTCT 202
      |||
Db     121 GCATCAGCAGTGGAGCGAGACCCGCTATCATGACCAACTGGCGGTGGCCGACCTCT 180
      |||
QY     203 GCCTGCTGTGCACCTTGGCCT 223
      |||
Db     181 GCCTGCTGTGCACCTTGGCCT 201
      |||

RESULT 12
US-10-741-600-61549
; Sequence 61549, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61549
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-61549

Query Match      21.6%; Score 200.6; DB 19; Length 201;
Best Local Similarity 99.5%; Pred. No. 4.7e-41;
Matches 200; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY     276 CCAGGCGCATCTACCTGACCAACAGGTACATGAGCATCAGCCTGGTCAAGCGCCATCGCCGT 335
      |||
Db      1 CCAGGCGCATCTACCTGACCAACAGGTACATGAGCATCAGCCTGGTCAAGCGCCATCGCCGT 60
      |||
QY     336 GGACCGCTATGTGGCGTGGCGCACCCGCTGGGTGCGCGGGCTGCGGTCCCGCCAGGCA 395
      |||
Db      61 GGACCGCTATGTGGCGTGGCGCACCCGCTGGGTGCGCGGGCTGCGGTCCCGCCAGGCA 120
      |||
QY     396 GCGTGGCGCGGTGCGCGGTCTCTGGGTGCTGCTATCGGCTCGCTGGTGGCTCGCTG 455
      |||
Db     121 GCGTGGCGCGGTGCGCGGTCTCTGGGTGCTGCTATCGGCTCGCTGGTGGCTCGCTG 180
      |||
QY     456 GCTCTCTGGGGATTTCAGGAGG 476
      |||
Db     181 GCTCTCTGGGGATTTCAGGAGG 201
      |||

RESULT 13
US-10-741-600-61551
; Sequence 61551, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61551
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-61551

Query Match      21.6%; Score 200.6; DB 19; Length 201;
Best Local Similarity 99.5%; Pred. No. 4.7e-41;
Matches 200; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY     276 CCAGGCGCATCTACCTGACCAACAGGTACATGAGCATCAGCCTGGTCAAGCGCCATCGCCGT 335
      |||
Db      1 CCAGGCGCATCTACCTGACCAACAGGTACATGAGCATCAGCCTGGTCAAGCGCCATCGCCGT 60
      |||
QY     336 GGACCGCTATGTGGCGTGGCGCACCCGCTGGGTGCGCGGGCTGCGGTCCCGCCAGGCA 395
      |||
Db      61 GGACCGCTATGTGGCGTGGCGCACCCGCTGGGTGCGCGGGCTGCGGTCCCGCCAGGCA 120
      |||
QY     396 GCGTGGCGCGGTGCGCGGTCTCTGGGTGCTGCTATCGGCTCGCTGGTGGCTCGCTG 455
      |||
Db     121 GCGTGGCGCGGTGCGCGGTCTCTGGGTGCTGCTATCGGCTCGCTGGTGGCTCGCTG 180
      |||
QY     456 GCTCTCTGGGGATTTCAGGAGG 476
      |||
Db     181 GCTCTCTGGGGATTTCAGGAGG 201
      |||

RESULT 14
US-10-741-600-61552
; Sequence 61552, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61552
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-61552

Query Match      21.6%; Score 200.6; DB 19; Length 201;
Best Local Similarity 99.5%; Pred. No. 4.7e-41;
Matches 200; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY     273 CTCACAGGCGCATCTACCTGACCAACAGGTACATGAGCATCAGCCTGGTCAAGCGCCATCGC 332
      |||
Db      1 CTCACAGGCGCATCTACCTGACCAACAGGTACATGAGCATCAGCCTGGTCAAGCGCCATCGC 60
      |||
QY     333 CQTGGACCGCTATGTGGCGCTGGCGCACCCGCTGGGTGCGCGGGCTGCGGTCCCGCCAG 392
      |||
Db      61 CQTGGACCGCTATGTGGCGCTGGCGCACCCGCTGGGTGCGCGGGCTGCGGTCCCGCCAG 120
      |||
QY     393 GCAGGCTGGCGCGGTGCGCGGTCTCTGGGTGCTGCTATCGGCTCGCTGGTGGCTCG 452
      |||
Db     121 GCAGGCTGGCGCGGTGCGCGGTCTCTGGGTGCTGCTATCGGCTCGCTGGTGGCTCG 180
      |||
QY     453 CTGGCTCTCTGGGGATTTCAGGA 473
      |||
Db     181 CTGGCTCTCTGGGGATTTCAGGA 201
      |||

RESULT 15
US-10-741-600-61567
; Sequence 61567, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
```

```
Query Match      21.6%; Score 200.6; DB 19; Length 201;
Best Local Similarity 99.5%; Pred. No. 4.7e-41;
Matches 200; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY     558 TGGGCGCAACCTCTCTGGGTGTTCTGCTGCTTCTTCCCTGCCCCCTGCACGTGGGGCTGACAGTG 717
      |||
Db      1 TGGGCGCAACCTCTCTGGGTGTTCTGCTGCTTCTTCCCTGCCCCCTGCACGTGGGGCTGACAGTG 60
      |||
QY     718 CGCCTCGCAGTGGGCTGGAAAGCCTGTGCCCTCTCTGGAGAGCATCCGTGCGGCCCTGTAC 777
      |||
Db      61 CGCCTCGCAGTGGGCTGGAAAGCCTGTGCCCTCTCTGGAGAGCATCCGTGCGGCCCTGTAC 120
      |||
QY     778 ATAAACCAAGCAAGCTCTCAGATGCCAACTGTGCCCTGCGCGCCATCTGCTACTACTACATG 837
      |||
Db     121 ATAAACCAAGCAAGCTCTCAGATGCCAACTGTGCCCTGCGCGCCATCTGCTACTACTACATG 180
      |||
QY     838 GCCAAGGAGTTCCAGGAGGCG 858
      |||
Db     181 GCCAAGGAGTTCCAGGAGGCG 201
      |||

RESULT 14
US-10-741-600-61552
; Sequence 61552, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61552
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-61552

Query Match      21.6%; Score 200.6; DB 19; Length 201;
Best Local Similarity 99.5%; Pred. No. 4.7e-41;
Matches 200; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY     273 CTCACAGGCGCATCTACCTGACCAACAGGTACATGAGCATCAGCCTGGTCAAGCGCCATCGC 332
      |||
Db      1 CTCACAGGCGCATCTACCTGACCAACAGGTACATGAGCATCAGCCTGGTCAAGCGCCATCGC 60
      |||
QY     333 CQTGGACCGCTATGTGGCGCTGGCGCACCCGCTGGGTGCGCGGGCTGCGGTCCCGCCAG 392
      |||
Db      61 CQTGGACCGCTATGTGGCGCTGGCGCACCCGCTGGGTGCGCGGGCTGCGGTCCCGCCAG 120
      |||
QY     393 GCAGGCTGGCGCGGTGCGCGGTCTCTGGGTGCTGCTATCGGCTCGCTGGTGGCTCG 452
      |||
Db     121 GCAGGCTGGCGCGGTGCGCGGTCTCTGGGTGCTGCTATCGGCTCGCTGGTGGCTCG 180
      |||
QY     453 CTGGCTCTCTGGGGATTTCAGGA 473
      |||
Db     181 CTGGCTCTCTGGGGATTTCAGGA 201
      |||

RESULT 15
US-10-741-600-61567
; Sequence 61567, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
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; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 61567  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-741-600-61567

Query Match 21.6%; Score 200.6; DB 19; Length 201;  
Best Local Similarity 99.5%; Pred. No. 4.7e-41;  
Matches 200; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 116 GCCTGGCGCTCTGGGTGTTCTGCTGCCGATGCGACGTGGACGGAGACCGCATCTACA 175  
Db 1 GCCTGGCGCTCTGGGTGTTCTGCTGCCGATGCGACGTGGACGGAGACCGCATCTACA 60  
Qy 176 TGACCAACCTGGCGGTGGCGACCTCTGCTGCTGTGCACCTTGCCCTTCGTGCTGCACT 235  
Db 61 TGACCAACCTGGCGGTGGCGACCTCTGCTGCTGTGCACCTTGCCCTTCGTGCTGCACT 120  
Qy 236 CCCTGGCGAGACCTTCAGACACGCGCTGTGCGCAGCTCTCCAGGGCATCTACCTGACCA 295  
Db 121 CCCTGGCGAGACCTTCAGACACGCGCTGTGCGCAGCTCTCCAGGGCATCTACCTGACCA 180  
Qy 296 ACAGTACATGAGCATCAGCC 316  
Db 181 ACAGTACATGAGCATCAGCC 201

Search completed: May 23, 2005, 14:50:03  
Job time : 2851 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 11:27:51 ; Search time 624 Seconds  
(without alignments)  
8822.691 Million cell updates/sec

Title: US-10-083-168-84

Perfect score: 930

Sequence: 1 atgaatgcacactacaacac.....tgtggtgacctgcctaa 930

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_16Dec04.\*

- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	930	100.0	930	6	ABST73401 DNA encod
2	925.2	99.5	930	6	ABST73345
3	925.2	99.5	930	8	ABZ42852 Human G p
4	925.2	99.5	930	9	ADb67672 Human G p
5	925.2	99.5	930	12	ADO29916 Human GPC
6	922	99.1	1369	3	AAZ50891 Human rec
7	920.4	99.0	1875	3	AAA27485 Human G p
8	920.4	99.0	1875	8	ADA84068 Human GPR
9	920.4	99.0	1875	12	ADO78086 Human GPR
10	920.4	99.0	49136	3	AAA27475 NIDDM1 re
11	919	98.8	1644	10	ADF70563 Orphan re
12	917.2	98.6	3811	13	ADR10415 Full leng
13	915.6	98.5	1043	3	AAZ35390 Human G p
14	900	96.8	1989	6	ABZ35525 Human gen
15	838	90.1	858	12	ADP28534 Human sec
16	549.2	59.1	924	12	ADO30206 Mouse GPC
17	141.8	15.2	1854	4	ADL10133 Mouse G p
18	141.8	15.2	1854	6	ABL35067 Murine cd
19	120.6	13.0	121	10	ADF87215 Single nu
20	111.6	12.0	1098	3	AAA30740 DNA encod

21	111.6	12.0	1098	10	ADC22744
22	111.6	12.0	1098	10	ADH14217
23	111.2	12.0	1089	3	AAA30581
24	111.2	12.0	1089	6	AAD26832
25	111.2	12.0	1089	8	ACC78113
26	111.2	12.0	1089	10	ADC22522
27	111.2	12.0	1089	10	ADH13995
28	111.2	12.0	1089	12	ADO23766
29	111.2	12.0	1365	6	ABZ34905
30	111.2	12.0	1365	10	ADE84894
31	111.2	12.0	1365	10	ACA56831
32	111.2	12.0	1365	12	ADI56627
33	111.2	12.0	2693	8	AAZ50858
34	111.2	12.0	2696	8	ABZ42741
35	111.2	12.0	2696	12	ADF17570
36	111.2	12.0	2696	12	ADO28684
37	111.2	12.0	2932	6	AAD26831
38	111.2	12.0	2932	12	ADL71938
39	111.2	12.0	2932	13	ADS19844
40	111.2	12.0	2980	6	ABZ35345
41	110.8	11.9	2932	6	AAD26878
42	110.6	11.9	121	10	ADF87214
43	110.4	11.9	970	2	AAZ10250
44	110.4	11.9	1149	5	AAZ88030
45	110.4	11.9	1617	3	AAZ95037

#### ALIGNMENTS

#### RESULT 1

ABS73401

ID ABS73401 standard; DNA; 930 BP.

AC ABS73401;

XX ABS73401;

DT 04-DEC-2002 (first entry)

DE DNA encoding human GPCR GPR35 mutant A216K.

KW Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy;  
KW hypertension; reflux disease; depression; migraine; schizophrenia; ulcer;  
KW psychotic disorder; asthma; bronchospasm; anaesthesia;  
KW myocardial infarction; MI; stroke; Glaucoma; anxiety;  
KW prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina;  
KW prostatic hypertrophy; mutant; ds.

OS Homo sapiens.

OS Synthetic.

XX WO200268600-A2.

PN WO200268600-A2.

PD 06-SEP-2002.

XX 26-FEB-2002; 2002WO-US005625.

XX 26-FEB-2001; 2001US-0271913P.

XX (AREN-) ARENA PHARM INC.

XX Liaw CW, Chalmers DT, Behan DP, Maciejewski-Lenior D, Leonard JN;  
XX Lin I, Ortuno D;

XX WPI; 2002-706980/76.

XX P-PSDB; ABC95172.

PT New human G-protein coupled receptor (GPCR), useful for screening agonist  
or inverse agonist compounds for treating diseases associated with GPCR.

XX Example 2; Page 188-189; 201pp; English.

XX The present invention relates to transmembrane receptors, particularly  
CC endogenous human G-protein coupled receptors (GPCRs), mutant (non-

CC endogenous) versions of the GPCR, and the polynucleotide sequences  
CC encoding them. The GPCRs are useful for screening agonist or inverse  
CC agonist compounds for treating diseases associated with GPCR. Diseases  
CC that can be treated with such compounds include allergies, hypertension,  
CC reflux disease, depression, migraine, schizophrenia, ulcers, psychotic  
CC disorders, asthma, bronchospasm, anaesthesia, myocardial infarction (MI),  
CC stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer,  
CC anxiety, prostatic hypertrophy, rhinitis, and angina. The present  
CC sequence encodes a mutant human GPCR  
XX  
SQ Sequence 930 BP; 141 A; 326 C; 278 G; 185 T; 0 U; 0 Other;

Query Match	100.0%;	Score 930;	DB 6;	Length 930;
Best Local Similarity	100.0%;	Pred. No. 1.9e-176;		
Matches 930;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ATGAATGGCACCTACACACCTCTACTTGGGCGTCTCTGGTTCAGAGGACCTCAGCTGGCCCCCAGCGATCAAG	60	
Db	1	ATGAATGGCACCTACACACCTGTGGTTCAGAGGACCTCACTGGCCCCCAGCGATCAAG	60	
Qy	61	CTGGGCTTCTACGGCTACTTCTGGGCGTCTCTGGTTCAGAGGACCTCAGCTGGCCCCCAGCGATCAAG	120	
Db	61	CTGGGCTTCTACGGCTACTTGGGCGTCTCTGGTTCAGAGGACCTCAGCTGGCCCCCAGCGATCAAG	120	
Qy	121	CGGCTCTGGGTTTCTGCTGCCGATGACGAGTGGACCGGACCCGATCTACATGACC	180	
Db	121	CGGCTCTGGGTTTCTGCTGCCGATGACGAGTGGACCGGACCCGATCTACATGACC	180	
Qy	181	AACCTGGGGTGGCGGACCTCTGCTGTGTGTCACCTTGCCTTCGTCTGCTGCACTCCCTG	240	
Db	181	AACCTGGGGTGGCGGACCTCTGCTGTGTGTCACCTTGCCTTCGTCTGCTGCACTCCCTG	240	
Qy	241	CGAGACACCTCAGACACGCGCTGTGCCAGCTCTCCAGGGGATCTACTGTGACCAACAGG	300	
Db	241	CGAGACACCTCAGACACGCGCGTGTGCCAGCTCTCCAGGGGATCTACTGTGACCAACAGG	300	
Qy	301	TACATGAGCATCAGCCTGGTCAACGGCCATCGCCGTGGACCCGATGTGGCCGTGCGGAC	360	
Db	301	TACATGAGCATCAGCCTGGTCAACGGCCATCGCCGTGGACCCGATGTGGCCGTGCGGAC	360	
Qy	361	CGGCTGGTGGCCCGGGGCTCGGGTCCCGCAGGACGAGGTGGCGCGTGTGGCGGTCCTC	420	
Db	361	CGGCTGGTGGCCCGGGGCTCGGGTCCCGCAGGACGAGGTGGCGCGTGTGGCGGTCCTC	420	
Qy	421	TGGGTGTGTGTTCATCGGCTCCCTGTGTGCTCGCTGGCTCTCGGGATTCAGAGAGGCGCG	480	
Db	421	TGGGTGTGTGTTCATCGGCTCCCTGTGTGCTCGCTGGCTCTCGGGATTCAGAGAGGCGCG	480	
Qy	481	TTCTGTCTCAGGAGCACCCGGACAAATTTCAAATTCATCGGATTCCTCGTGGGATTC	540	
Db	481	TTCTGTCTCAGGAGCACCCGGACAAATTTCAAATTCATCGGATTCCTCGTGGGATTC	540	
Qy	541	TACCTGGCCCTGGCGTGGTCTTCTGTCTCCCTGAAGGTGGTGACTGCCCTGGGCCCG	600	
Db	541	TACCTGGCCCTGGCGTGGTCTTCTGTCTCCCTGAAGGTGGTGACTGCCCTGGGCCCG	600	
Qy	601	AGGCCACCCACGAGTGGGCGAGGACGAGCCACCCGACAGGCTAAACGATGTCGTCGG	660	
Db	601	AGGCCACCCACGAGTGGGCGAGGACGAGCCACCCGACAGGCTAAACGATGTCGTCGG	660	
Qy	661	GCCAACTCTCTGGTGTCTGGTCTGTCTCTGTGCCCTTCACGTGGGGCTGACAGTGCGC	720	
Db	661	GCCAACTCTCTGGTGTCTGGTCTGTCTCTGTGCCCTTCACGTGGGGCTGACAGTGCGC	720	
Qy	721	CTCGAGTGGGCTGGAACGCTGTGCCCTCTCTGTGAGACGATCCGCTGGCCCTGTACATA	780	
Db	721	CTCGAGTGGGCTGGAACGCTGTGCCCTCTCTGTGAGACGATCCGCTGGCCCTGTACATA	780	
Qy	781	ACGACGAGCTCTCAGATGACCACTGCTGCTCGCTGGAGCCATCTGCTACTTACATGGCC	840	
Db	781	ACGACGAGCTCTCAGATGACCACTGCTGCTCGCTGGAGCCATCTGCTACTTACATGGCC	840	
Qy	841	AAGGAGTTTCAGAGGCGCTCTGCACTGGCCGTGGCTCCCGTGTCTAAGGCCCAACAAAGC	900	

Db	841	AAGGAGTTCAGAGGCGCTGCACTGCGCGTGGCTCCCCGTGTAGGCCCAAAAGC	900
QY	901	CAGGACTCTCTGTGCGTGACCCCTGCCTAA	930
Db	901	CAGGACTCTCTGTGCGTGACCCCTGCCTAA	930
RESULT 2			
ABS73345			
ID	ABS73345 standard; cDNA; 930 BP.		
XX	AC	ABS73345;	
XX	DT	04-DEC-2002 (first entry)	
XX	DE	cDNA encoding human GPCR GPR35.	
XX	KW	Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy;	
KW	KW	hypertension; reflux disease; depression; migraine; schizophrenia; ulcer;	
KW	KW	psychotic disorder; asthma; bronchospasm; anaesthesia;	
KW	KW	myocardial infarction; MI; stroke; glaucoma; anxiety;	
KW	KW	prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina;	
XX	XX	prostatic hypertrophy; gene; ss.	
OS	Homo sapiens.		

XX WC200268600-A2.  
XX  
XX  
XX PD 06-SEP-2002.  
XX  
XX 26-FEB-2002; 2002WO-US0005625.  
XX  
XX 26-FEB-2001; 2001US-0271913P.  
XX  
XX (AREN-) ARENA PHARM INC.  
XX  
XX Liaw CW, Chalmers DT, Behan DP, Maciejewski-Lenior D, Leonard JN;  
XX Lin I, Ortuno D;  
XX  
XX WPI: 2002-706980/76.  
XX P-PSDB; ABG95159.  
XX  
XX  
XX New human G-protein coupled receptor (GPCR), useful for screening agonist  
XX or inverse agonist compounds for treating diseases associated with GPCR.  
XX  
XX Claim 31; Page 128; 201pp; English.  
XX PS

XX  
CC The present invention relates to transmembrane receptors, particularly  
CC endogenous human G-protein coupled receptors (GPCRs), mutant (non-  
CC endogenous) versions of the GPCRs, and the polynucleotide sequences  
CC encoding them. The GPCRs are useful for screening agonist or inverse  
CC agonist compounds for treating diseases associated with GPCR. Diseases  
CC that can be treated with such compounds include allergies, hypertension,  
CC reflux disease, depression, migraine, schizophrenia, ulcers, psychotic  
CC disorders, asthma, bronchospasm, anaesthesia, myocardial infarction (MI),  
CC stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer,  
CC anxiety, prostatic hypertrophy, rhinitis, and angina. The present  
CC sequence encodes an endogenous human GPCR

XX	Sequence 930 BP; 138 A; 328 C; 279 G; 185 T; 0 U; 0 Other;	
SQ	Query Match 99.5%; Score 925.2; DB 6; Length 930;	
	Best Local Similarity 99.7%; Pred. No. 1.7e-175;	
	Matches 927; Conservative 0; Mismatches 3; Indels 0; Gaps 0	

Qy	1	ATGAATGGCACCTTACAACACCTGTGGCTCCAGCGACCTCAGCTGGCCCCCAGCGATCAAG	60
Db <td>1 <td>ATGAATGGCACCTTACAACACCTGTGGCTCCAGCGACCTCAGCTGGCCCCCAGCGATCAAG <td>60</td> </td></td>	1 <td>ATGAATGGCACCTTACAACACCTGTGGCTCCAGCGACCTCAGCTGGCCCCCAGCGATCAAG <td>60</td> </td>	ATGAATGGCACCTTACAACACCTGTGGCTCCAGCGACCTCAGCTGGCCCCCAGCGATCAAG <td>60</td>	60
Qy <td>61 <td>CTGGGCTTCTACGCTACTATTGGGCGTCTGTGTGTGTAGGCTCTGCTCAACAGCCTTG <td>120</td> </td></td>	61 <td>CTGGGCTTCTACGCTACTATTGGGCGTCTGTGTGTGTAGGCTCTGCTCAACAGCCTTG <td>120</td> </td>	CTGGGCTTCTACGCTACTATTGGGCGTCTGTGTGTGTAGGCTCTGCTCAACAGCCTTG <td>120</td>	120
Db <td>61 <td>CTGGGCTTCTACGCTACTATTGGGCGTCTGTGTGTGTAGGCTCTGCTCAACAGCCTTG <td>120</td> </td></td>	61 <td>CTGGGCTTCTACGCTACTATTGGGCGTCTGTGTGTGTAGGCTCTGCTCAACAGCCTTG <td>120</td> </td>	CTGGGCTTCTACGCTACTATTGGGCGTCTGTGTGTGTAGGCTCTGCTCAACAGCCTTG <td>120</td>	120





Db 601 AGGCACCCACGACGTGGGAGAGGAGGACCCGACAGGCTGCCGCGATGCTCTGG 660  
 Qy 661 GCCAACCTCTGGTGTTCGTGTCTGCTTCTGCTCCCTGACAGTGGGCTGACAGTGGC 720  
 Db 661 GCCAACCTCTGGTGTTCGTGTCTGCTTCTGCTCCCTGACAGTGGGCTGACAGTGGC 720  
 Qy 721 CTCGAGTGGGCTGGAAGCCCTGTGCCCTCTGAGAGCATCCGTCGCGCCCTGTACATA 780  
 Db 721 CTCGAGTGGGCTGGAAGCCCTGTGCCCTCTGAGAGCATCCGTCGCGCCCTGTACATA 780  
 Qy 781 ACCAGCAAGCTCTCAGATGCCAATCTGCTGCTGAGCGCCATCTGCTACTTACATGGCC 840  
 Db 781 ACCAGCAAGCTCTCAGATGCCAATCTGCTGCTGAGCGCCATCTGCTACTTACATGGCC 840  
 Qy 841 AAGGAGTTCAGGAGCGCTGTGCATCTGCGCTGCGCTCCCGTGTAAAGCCCAAAAGC 900  
 Db 841 AAGGAGTTCAGGAGCGCTGTGCATCTGCGCTGCGCTCCCGTGTAAAGCCCAAAAGC 900  
 Qy 901 CAGGACTCTGTGTGCTGACCTCGCCTAA 930  
 Db 901 CAGGACTCTGTGTGCTGACCTCGCCTAA 930

## RESULT 5

ADO29916

ID ADO29916 standard; cDNA; 930 BP.

XX AC ADO29916;

XX DT 29-JUL-2004 (first entry)

XX DE Human GPCR GPR35 polynucleotide, SEQ ID NO:1018.

XX KW G protein-coupled receptor; GPCR; drug screening; diagnosis;

XX KW transgenic mouse; neurological disorder; adrenal gland disorder;

XX KW colon disorder; intestinal disorder; cardiovascular disorder;

XX KW muscular disorder; blood disorder; immune disorder; bone disorder;

XX KW joint disorder; metabolic disorder; nutritive disorder; cancer;

XX KW kidney disorder; liver disorder; lung disorder; breast disorder;

XX KW ovary disorder; stomach disorder; prostate disorder; testis disorder;

XX KW skin disorder; thyroid disorder; pancreas disorder; spleen disorder;

XX KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;

XX KW cytosolic; antiinflammatory; vasotropic; antiangular; antiarrhythmic;

XX KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;

XX KW viricide; hepatotropic; antibacterial; antianemic; antiseborrhoeic;

XX KW dermatological; antitumor; antithyroid; antiallergic; anorectic;

XX KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;

XX KW gene; ss.

XX OS Homo sapiens.

XX PN WO2004040000-A2.

XX PD 13-MAY-2004.

XX PF 09-SEP-2003; 2003WO-US028226.

XX PR 09-SEP-2002; 2002US-0409103P.

XX PR 09-APR-2003; 2003US-0461329P.

XX PA (PRIM-) PRIMAL INC.

XX PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;

XX PI Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;

XX DR WPI; 2004-390329/36.

XX DR P-PSDB; ADO29916.

XX PT Novel mammalian G protein coupled receptors, useful for identifying

XX PT compounds that modulates diagnosing and treating disease condition

XX PT associated with GPCR dysfunction e.g. autoimmune diseases, angina

XX PT pectoris, Parkinson's disease.

XX PT

PS Claim 151; SEQ ID NO 1018; 542pp; English.

XX The invention relates to human and mouse G protein-coupled receptors (GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention; methods of treating, preventing or diagnosing diseases associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic mouse comprising a GPCR gene of the invention; a mouse comprising a mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived from the transgenic mice; kits comprising several mice, each of which has a mutation in a different GPCR gene of the invention; and kits comprising probes which hybridise to GPCR polynucleotides of the invention. The invention further discloses variants of the GPCR polypeptides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, depression, diabetic neuropathy, Parkinson's disease or schizophrenia); disorders of the adrenal gland; disorders of the colon or intestine (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or myocardial infarction); muscular disorders; blood disorders (e.g., anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g., obesity, enzyme deficiency-related diseases or vitamin deficiency-related diseases); and disorders of the kidney, liver, lung, breast, ovary, uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and thyroid (e.g., cancers). The present sequence represents a GPCR-encoding nucleic acid of the invention. Note: The full sequence data for this patent did not form part of the printed specification; those sequences not shown were obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

SQ Sequence 930 BP; 138 A; 328 C; 279 G; 185 T; 0 U; 0 Other;

Query Match 99.5%; Score 925.2; DB 12; Length 930;

Best Local Similarity 99.7%; Pred. No. 1.7e-175;

Matches 927; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGAATGCACCTACAACACCTGTGGCTCCAGGACCTCACCTGCCCCACGATCAAG 60

Db 1 ATGAATGCACCTACAACACCTGTGGCTCCAGGACCTCACCTGCCCCACGATCAAG 60

Qy 61 CTGGGCTTCTACGCCCTACTTGGGCGTCTCTGTGGTGTAGGCTCTGCTCAACGCTTG 120

Db 61 CTGGGCTTCTACGCCCTACTTGGGCGTCTCTGTGGTGTAGGCTCTGCTCAACGCTTG 120

Qy 121 GCGCTCTGGGTGTTCTGTGCGGCATGCGAGTGGACGGACCCGATCTACATGACC 180

Db 121 GCGCTCTGGGTGTTCTGTGCGGCATGCGAGTGGACGGACCCGATCTACATGACC 180

Qy 181 AACCTGGCGGTGGCGACCTCTGCTGTGTGACCTTGGCTTGTGCTGACCTCCCTG 240

Db 181 AACCTGGCGGTGGCGACCTCTGCTGTGTGACCTTGGCTTGTGCTGACCTCCCTG 240

Qy 241 CGAGACACCTCAGACACCGCGCTGTGCCAGCTCTCCAGGGCATCTACTGACCAACAG 300

Db 241 CGAGACACCTCAGACACCGCGCTGTGCCAGCTCTCCAGGGCATCTACTGACCAACAG 300

Qy 301 TACATGAGCATCAGCTTGGTCAAGCCATCGCGTGGACCGCTATGTGGCCGTGGCGCAC 360

Db 301 TACATGAGCATCAGCTTGGTCAAGCCATCGCGTGGACCGCTATGTGGCCGTGGCGCAC 360

Qy 361 CCGCTGCTGCGCCGCGGCTGGGTCGCCAGGAGGCTGGGCGGTGGCGGTCTCTC 420

Db 361 CCGCTGCTGCGCCGCGGCTGGGTCGCCAGGAGGCTGGGCGGTGGCGGTCTCTC 420

Qy 421 TGGGTGCTGCTCATCGGCTCCCTGTGGTGTGCTGCTGCTGGGATTCAGAGGCGCGC 480

Db 421 TGGGTGCTGCTCATCGGCTCCCTGTGGTGTGCTGCTGCTGGGATTCAGAGGCGCGC 480

Qy 481 TTCTGCTTTCAGAGCACCCCGGCACAAATTTCAATCTCAATGCGGTTCCTCCGCTGCTGGGATTC 540







QY 781 ACCAGAGCTCTCAGATGCCAACTGCTGCTGGAGCGCATCTGCTACTACTACATGGCC 840  
Db 1356 ACCAGAGCTCTCAGATGCCAACTGCTGCTGGAGCGCATCTGCTACTACTACATGGCC 1415  
QY 841 AAGGAGTTCCAGGAGCGGTCTGCACCTGGGCGGTGCTCCCGTGTAAAGGCCACAAAAAGC 900  
Db 1416 AAGGAGTTCCAGGAGCGGTCTGCACCTGGGCGGTGCTCCCGTGTAAAGGCCACAAAAAGC 1475  
QY 901 CAGGACTCTCTGTGGTGACCTTCGGCTAA 930  
Db 1476 CAGGACTCTCTGTGGTGACCTTCGGCTAA 1505

RESULT 8

ADA84068  
ID ADA84068 standard; DNA; 1875 BP.

AC ADA84068;

DT 20-NOV-2003 (first entry)

XX Human GPR35 gene.

DE human; marker; expressed sequence tag; EST; arabidopsis; tumour;

KW stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;

KW vaccine; ds; gene.

XX Homo sapiens.

XX WO2002103028-A2.

XX 27-DEC-2002.

XX 30-MAY-2002; 2002WO-IB004189.

XX 30-MAY-2001; 2001US-0293999P.

PR 22-OCT-2001; 2001US-0330457P.

PR 19-FEB-2002; 2002US-0357144P.

XX (BIOW-) BIOMEDICAL CENT.

XX Baranova AV, Yankovsky NK, Kozlov AP, Lobashev AV, Krukovskaya LL;

XX WPI; 2003-175241/17.

DR P-PSDB; ADA84069.

XX Determining if a nucleic acid is a marker for a phenotype/cell type of interest, by global comparison of expressed sequence tags known to be expressed in the phenotype/cell type with all ESTs expressed in normal tissue.

XX Claim 23; Page 446-448; 516pp; English.

XX The invention relates to a novel method for determining if a nucleic acid is a marker for a predetermined phenotype/cell type of interest from a biological species. The method comprises performing a global comparison of a group of expressed sequence tags (ESTs) known to be expressed in the phenotype/cell type of interest with all ESTs expressed in normal tissue in order to identify ESTs that are preferentially expressed in the phenotype/cell of interest. A method of the invention is useful for determining whether a nucleic acid is a marker for a predetermined phenotype or cell type of interest from a biological species, preferably Arabidopsis or human. The cell type of interest is an abnormal cell such as a tumour cell, and the predetermined phenotype is a stress-induced phenotype such as hyperosmotic stress or high salt conditions. A method of the invention is also useful for determining the progression of colon cancer in a human, for detecting a tumour cell, and for regulating or preventing the growth of a tumour cell. An antibody of the invention is useful for detecting the absence or presence of peptides encoded by tumour-associated markers. A polypeptide of the invention is useful as an immunogen for vaccinating an animal. The present sequence encodes a tumour-associated antigen of the invention.

XX SQ Sequence 1875 BP; 290 A; 593 C; 614 G; 378 T; 0 U; 0 Other;  
Query Match 99.0%; Score 920.4; DB 8; Length 1875;  
Best Local Similarity 99.4%; Pred. No. 1.7e-174;  
Matches 924; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 ATGAATGCACCTACAACACACCTGTGGCTCCAGCGACCTCACCTGGCCCCCAGCGATCAAG 60  
Db 576 ATGAATGCACCTACAACACCTGTGGCTCCAGCGACCTCACCTGGCCCCCAGCGATCAAG 635  
QY 61 CTGGCTTTTACGCTACTTGGGGCTCTGTGGTGTAGGCTCTGCTCAACAGCCTG 120  
Db 636 CTGGCTTTTACGCTACTTGGGGCTCTGTGGTGTAGGCTCTGCTCAACAGCCTG 695  
QY 121 CGGCTCTGGGTGTTCTGTGCGGCATGCAGCAGTGGACGGAGACCGCATCTACATGACC 180  
Db 696 GCGCTCTGGGTGTTCTGTGCGGCATGCAGCAGTGGACGGAGACCGCATCTACATGACC 755  
QY 181 AACCTGGGGTGGCGACCTCTGCTGCTGTGTGACCTTTGCCCTTCTGCTGCTGCACTCCCTG 240  
Db 756 AACCTGGGGTGGCGACCTCTGCTGCTGTGTGACCTTTGCCCTTCTGCTGCTGCACTCCCTG 815  
QY 241 CGAGACCTCAGACACCGCGCTGTGCCAGCTTCTCCAGGGCATCTACTGACCAACAGG 300  
Db 816 CGAGACCTCAGACACCGCGCTGTGCCAGCTTCTCCAGGGCATCTACTGACCAACAGG 875  
QY 301 TACATGAGCATGAGCTGTGTCA CGGCCATGCCGTGGACCGCTATGTGGCGGTGCGGCAC 360  
Db 876 TACATGAGCATGAGCTGTGTCA CGGCCATGCCGTGGACCGCTATGTGGCGGTGCGGCAC 935  
QY 361 CGGCTGGCTGGCGCGGGCTCGCGTCCCGCAGGAGGCTGGCGGCGTGTGGCGGTCTCTC 420  
Db 936 CGGCTGGCTGGCGCGGGCTCGCGTCCCGCAGGAGGCTGGCGGCGTGTGGCGGTCTCTC 995  
QY 421 TGGGTGCTGGTCACTCGGCTCCCTGCTGCTGCTCGCTCTGGGGAATTCAGAGGGCGGC 480  
Db 996 TGGGTGCTGGTCACTCGGCTCCCTGCTGCTGCTCGCTCTGGGGAATTCAGAGGGCGGC 1055  
QY 481 TTCTGCTTCAGAGACACCGGCACTTCAACTCCATCGGTTCCCGTGTCTGGGATTC 540  
Db 1056 TTCTGCTTCAGAGACACCGGCACTTCAACTCCATCGGTTCCCGTGTCTGGGATTC 1115  
QY 541 TACCTGCCCTTCGGCGCTGCTGCTCTGCTCCCTGAAAGTGTGTGACTGCGCCCTGGCCCCAG 600  
Db 1116 TACCTGCCCTTCGGCGCTGCTGCTCTGCTCCCTGAAAGTGTGTGACTGCGCCCTGGCCCCAG 1175  
QY 601 AGGCCACCCACCGACGCTGGGGCAGGACGAGCGCACCCCGCAAGGCTTAAACGCATGTTGG 660  
Db 1176 AGGCCACCCACCGACGCTGGGGCAGGACGAGCGCACCCCGCAAGGCTTAAACGCATGTTGG 1235  
QY 661 GCCAACCTCTCTGGTGTCTGCTGCTTCTGCTCCCTGCGAGCTGGGGCTGACAGTGGCG 720  
Db 1236 GCCAACCTCTCTGGTGTCTGCTGCTTCTGCTCCCTGCGAGCTGGGGCTGACAGTGGCG 1295  
QY 721 CTCGAGTGGGCTGGAACGCTGCTGCCCTCTCTGGAGAGCATCCGTCGCGCCCTGTACATA 780  
Db 1296 CTCGAGTGGGCTGGAACGCTGCTGCCCTCTCTGGAGAGCATCCGTCGCGCCCTGTACATA 1355  
QY 781 ACCCAACAAGCTCTCAGATGCCAACTGTGCTGCTGGACCGCATCTGCTACTACTATGGCC 840  
Db 1356 ACCCAACAAGCTCTCAGATGCCAACTGTGCTGCTGGACCGCATCTGCTACTACTATGGCC 1415  
QY 841 AAGGAGTTCCAGGAGCGGTCTGCACCTGGCGGTGGCTCCCGTGTAAAGGCCACAAAAAGC 900  
Db 1416 AAGGAGTTCCAGGAGCGGTCTGCACCTGGCGGTGGCTCCCGTGTAAAGGCCACAAAAAGC 1475  
QY 901 CAGGACTCTCTGTGGTGACCTTCGGCTAA 930  
Db 1476 CAGGACTCTCTGTGGTGACCTTCGGCTAA 1505



AD078086  
 ID AD078086 standard; DNA; 1875 BP.  
 XX AC AD078086;  
 XX DT 26-AUG-2004 (first entry)  
 XX DE Human GPR35 DNA.  
 XX ds; gene; tumour-associated antigen; TAG; cancer; lung cancer;  
 KW breast cancer; prostate cancer; colon cancer; stomach cancer;  
 KW pancreatic cancer; ear cancer; nose cancer; throat cancer; kidney cancer;  
 KW cervical cancer; melanoma; tumour; human; GPR35.  
 XX OS Homo sapiens.  
 XX PN DE10254601-A1.  
 XX PD 03-JUN-2004.  
 XX PF 22-NOV-2002; 2002DE-01054601.  
 XX PR 22-NOV-2002; 2002DE-01054601.  
 XX PA (GANY-) GANYMED PHARM AG.  
 XX PI Tuerceci O, Sahin U, Koslowski M;  
 XX DR WPI; 2004-421820/40.  
 XX DR P-PSDB; AD078094.  
 XX Composition containing inhibitor of expression or activity of specific  
 PT tumor-associated antigens, useful for treating cancers, also related  
 PT compositions for diagnosis and monitoring.  
 XX Claim 1; SEQ ID NO 1; 124pp; German.  
 XX The invention relates to pharmaceutical compositions that comprise an  
 CC agent that inhibits the expression or activity of a tumour-associated  
 CC antigen (TAG) that is encoded by a nucleic acid. The pharmaceutical  
 CC compositions and related compositions, are used for treatment of diseases  
 CC associated with (abnormal) expression of TAG, specifically cancer e.g. of  
 CC lung, breast, prostate, colon, stomach, pancreas, ear/nose/throat, kidney  
 CC or cervix, also melanoma. Compositions containing TAG, or related nucleic  
 CC acid, antibodies or host cells, are also useful for diagnosis and  
 CC monitoring of tumours. The present sequence represents the human GPR35  
 CC DNA.  
 XX SQ Sequence 1875 BP; 290 A; 593 C; 614 G; 378 T; 0 U; 0 Other;  
 Query Match 99.0%; Score 920.4; DB 12; Length 1875;  
 Best Local Similarity 99.4%; Pred. No. 1.7e-174;  
 Matches 924; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 ATGAATGGACCTACAAACCTGTGGCTCCAGCGACCTACCTGGCCCCCAGCGATCAAG 60  
 Db 576 ATGAATGGACCTACAAACCTGTGGCTCCAGCGACCTACCTGGCCCCCAGCGATCAAG 635  
 QY 61 CTGGGCTTCTAGCCTACTTGGGCGTCTGTGGTCTAGGCTGCTGCTCAACGCTG 120  
 Db 636 CTGGGCTTCTAGCCTACTTGGGCGTCTGTGGTCTAGGCTGCTGCTCAACGCTG 695  
 QY 121 GGGCTCTGGGTGTTCTGTCTGCCGATGACGAGAGCCGCGATCTACATGACC 180  
 Db 696 GGGCTCTGGGTGTTCTGTCTGCCGATGACGAGAGCCGCGATCTACATGACC 755  
 QY 181 AACCTGGGGTGGCGGACCTCTGCTGTGTGACCTTTGCCCTTGTGTGCTGCACTCCCTG 240  
 Db 756 AACCTGGGGTGGCGGACCTCTGCTGTGTGACCTTTGCCCTTGTGTGCTGCACTCCCTG 815  
 QY 241 CGAGACACCTCAGACACGCGGCTGTGCGAGCTCTCCAGGGGATCTACTGACCAACAGG 300  
 Db 816 CGAGACACCTCAGACACGCGGCTGTGCGAGCTCTCCAGGGGATCTACTGACCAACAGG 875

QY 301 TACATGAGCATCAGCCTGGTCA CGGCCATCGCCCTATGTCGCGCTGCGGCAC 360  
 Db 876 TACATGAGCATCAGCCTGGTCA CGGCCATCGCCCTATGTCGCGCTGCGGCAC 935  
 QY 361 CGCTGTGCTGCCCGGGCTGCGGTC CCCCAGGAGGCTGCGGGCGGTGTGCGCGGTCTTC 420  
 Db 936 CGCTGTGCTGCCCGGGCTGCGGTC CCCCAGGAGGCTGCGGGCGGTGTGCGCGGTCTTC 995  
 QY 421 TGGGTGCTGGTCATCGGCTCCCTGT GGTGCTCGCTGGCTCTCTGGGATTCAGAGGCGCGC 480  
 Db 996 TGGGTGCTGGTCATCGGCTCCCTGT GGTGCTCGCTGGCTCTCTGGGATTCAGAGGCGCGC 1055  
 QY 481 TTCTGCTTCAGAGCACCGGCGACAAT TCACTCATGCGGTTCCCGTGTGCGGATTC 540  
 Db 1056 TTCTGCTTCAGAGCACCGGCGACAAT TCACTCATGCGGTTCCCGTGTGCGGATTC 1115  
 QY 541 TACCTGCCCTTGGCGGTGGTGTCTTC TGTCTCCCTGAAAGGTGGTGACTGCCCTGCGCCAG 600  
 Db 1116 TACCTGCCCTTGGCGGTGGTGTCTTC TGTCTCCCTGAAAGGTGGTGACTGCCCTGCGCCAG 1175  
 QY 601 AGGCCACCCACGACGTGGGCGAGCAG AGGCGCACCCGCAAGGCTAAACGCATGTCTGG 660  
 Db 1176 AGGCCACCCACGACGTGGGCGAGCAG AGGCGCACCCGCAAGGCTAAACGCATGTCTGG 1235  
 QY 661 GCCAACCTCTGTGGTGTGGTGTCTGTG TCTTCTGCCCCCTGCAGCTGGGGCTGACAGTGGC 720  
 Db 1236 GCCAACCTCTGTGGTGTGGTGTCTGTG TCTTCTGCCCCCTGCAGCTGGGGCTGACAGTGGC 1295  
 QY 721 CTGCGAGTGGGCTGGAGCGCTGTGCCCT CCTGGAGAGCATCCGTCGCGCCCTGTACATA 780  
 Db 1296 CTGCGAGTGGGCTGGAGCGCTGTGCCCT CCTGGAGAGCATCCGTCGCGCCCTGTACATA 1355  
 QY 781 ACCAGCAAGCTCTCAGATGCCAACACT GTGCTGCGCTGGAGCGCATCTGCTACTACTACATGGCC 840  
 Db 1356 ACCAGCAAGCTCTCAGATGCCAACACT GTGCTGCGCTGGAGCGCATCTGCTACTACTACATGGCC 1415  
 QY 841 AAGGAGTTCAGGAGGCGCTCTGCACTGG CCGGTGGCTTCCCGGTCTAAGGCCCAACAAAGC 900  
 Db 1416 AAGGAGTTCAGGAGGCGCTCTGCACTGG CCGGTGGCTTCCCGGTCTAAGGCCCAACAAAGC 1475  
 QY 901 CAGGACTCTCTGTGGCTGACCCCTGCGCCTAA 930  
 Db 1476 CAGGACTCTCTGTGGCTGACCCCTGCGCCTAA 1505  
 RESULT 10  
 ID AAA27475 standard; DNA; 49136 BP.  
 XX AC AAA27475;  
 XX DT 15-AUG-2000 (first entry)  
 XX DE NIDDM1 region including CAPN10 and GPR35 genes.  
 XX NIDDM1; non-insulin-dependent diabetes mellitus; CAPN10 gene; calpain 10;  
 KW GPR35 gene; G protein coupled receptor; human; polymorphism; UCSNP-43;  
 KW chromosome 2; diapain-1; diagnosis; therapy; ds.  
 XX OS Homo sapiens.  
 XX Key Location/Qualifiers  
 FH 1235..1515  
 exon /tag= a  
 FT /number= 1  
 FT /codon\_start= 1375  
 FT 1516..3812  
 intron /tag= b  
 FT /number= 1  
 FT 3813..3944  
 exon /tag= c  
 FT /number= 2

FT intron 3945. .5282  
 FT /tag= d  
 FT /number= 2  
 FT exon 5283. .5479  
 FT /tag= e  
 FT /number= 3  
 FT exon 5283. .5468  
 FT /tag= f  
 FT /number= 3\*  
 FT intron 5469. .6400  
 FT /tag= h  
 FT /number= 3\*  
 FT intron 5480. .6400  
 FT /tag= g  
 FT /number= 3  
 FT variation replace(6225,a)  
 FT /tag= ag  
 FT /frequency= "0.75"  
 FT /note= "G-allele has a frequency of 0.75 in Mexican  
 FT Americans"  
 FT /frequency= "0.71"  
 FT /note= "G-allele has a frequency of 0.71 in non-Hispanic  
 FT whites of German ancestry"  
 FT /frequency= "0.90"  
 FT /note= "G-allele has a frequency of 0.90 in African  
 FT Americans"  
 FT /frequency= "0.94"  
 FT /note= "G-allele has a frequency of 0.94 in Asians  
 FT (Japanese)"  
 FT 6401. .6618  
 FT /tag= i  
 FT /number= 4  
 FT intron 6619. .8372  
 FT /tag= j  
 FT /number= 4  
 FT exon 8373. .8514  
 FT /tag= k  
 FT /number= 5  
 FT intron 8515. .9009  
 FT /tag= l  
 FT /number= 5  
 FT exon 9010. .9175  
 FT /tag= m  
 FT /number= 6  
 FT /note= "TGA, 9013. .9015"  
 FT 9176. .9490  
 FT /tag= n  
 FT /number= 6  
 FT exon 9491. .9771  
 FT /tag= o  
 FT /number= 7  
 FT intron 9772. .10399  
 FT /tag= p  
 FT /number= 7  
 FT exon 10400. .10618  
 FT /tag= q  
 FT /number= 8  
 FT /note= "TGA, 10455. .10457"  
 FT 10619. .10784  
 FT /tag= r  
 FT /number= 8  
 FT exon 10785. .10987  
 FT /tag= s  
 FT /number= 9  
 FT intron 10988. .11146  
 FT /tag= t  
 FT /number= 9  
 FT exon 11147. .11408  
 FT /tag= u  
 FT /number= 10  
 FT exon 11316. .11408  
 FT /tag= v  
 FT /number= 10\*

FT intron 11409. .12353  
 FT /tag= w  
 FT /number= 10  
 FT exon 12354. .12553  
 FT /tag= x  
 FT /number= 11  
 FT /note= "TGA, 12412. .12414"  
 FT 12554. .12817  
 FT /tag= y  
 FT /number= 11  
 FT exon 12818. .12863  
 FT /tag= z  
 FT /number= 12  
 FT intron 12864. .13116  
 FT /tag= aa  
 FT /number= 12  
 FT exon 13117. .13569  
 FT /tag= ab  
 FT /number= 13  
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 FT 13570. .30856  
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 FT /number= 13  
 FT exon 30857. .30980  
 FT /tag= ad  
 FT /number= 14  
 FT intron 30981. .31445  
 FT /tag= ae  
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 FT exon 31446. .32175  
 FT /tag= af  
 FT /number= 15  
 FT CDS 43070. .44944  
 FT /tag= ah  
 FT /note= "encodes GPR35 (AAV79576)"  
 FT 44922. .44927  
 FT /tag= ai  
 FT polyA\_signal  
 FT WO200023603-A2.  
 PN 27-APR-2000.  
 PD 21-OCT-1999; 99WO-US024890.  
 XX 21-OCT-1998; 98US-0105052P.  
 PR 13-MAY-1999; 99US-0134175P.  
 PR (ARCH-) ARCH DEV CORP.  
 PA (TEXA ) UNIV OF TEXAS SYSTEM.  
 PA Polonsky KS, Horikawa Y, Oda N, Sreenan S, Zhou Y, Otani K;  
 PI Hanis CL, Bell GI, Cox NJ;  
 PI WPI; 2000-339702/29.  
 DR P-PSDB; AAV79567, AAV79568, AAV79569, AAV79570, AAV79571, AAV79572,  
 DR AAV79573, AAV79574, AAV79576.  
 XX Method for screening for type 2 diabetes mellitus comprises detecting a  
 FT polymorphism in a calpain encoding nucleic acid segment or a protease-  
 FT encoding nucleic acid segment.  
 PT Claim 65; Page 203-217; 257pp; English.  
 PS The present sequence is that of a 49,136 bp region located within the  
 CC NIDDM1 region of human chromosome 2. It includes the CAPN10 gene that  
 CC encodes a novel calpain-like cysteine protease, designated calpain 10,  
 CC and a gene encoding a G protein coupled receptor, GPR35. Alternative  
 CC splicing of calpain 10 mRNA generates a family of proteins. Isoforms 10a-  
 CC h (see AAV79567-74) are respectively encoded by exons 1-7,9-13, 1-  
 CC 7,9,10\*,11-13, 1-7,11-13, 1-7,9,11-13, 1-10\*,11-13, 1-3\*,4-7,9-13, 1-  
 CC 1,2,14,15 and 1,11-13. Calpain 10 mRNA is ubiquitously expressed; the  
 CC major 2.7 kb transcript was detected in every human adult and foetal  
 CC tissue examined. Mutations in the CAPN10 gene are responsible for

CC susceptibility to type 2 diabetes. The nucleotide variant showing all the  
CC evidence for linkage to type 2 diabetes, UCSNP-43, is located at  
CC nucleotide 6225 in intron 3 of the gene. There is alternative splicing of  
CC intron 3, but the molecular mechanism by which the polymorphism at UCSNP-  
CC 43 affects susceptibility to type 2 diabetes is unclear. Claimed methods  
CC for screening for a propensity for type 2 diabetes mellitus are based on  
CC detection of a polymorphism in a calpain encoding nucleic acid,  
CC especially UCSNP-10 of the CAPN10 gene. Methods are also claimed for  
CC identifying modulators of calpain activity using calpain 10 polypeptides  
CC and nucleic acids, and using these modulators to treat diabetes, in  
CC particular through the regulation of an insulin secretory response or  
CC insulin mediated glucose transport  
XX  
XX  
SQ Sequence 49136 BP; 10300 A; 13118 C; 14165 G; 11553 T; 0 U; 0 Other;

Query Match 99.0%; Score 920.4; DB 3; Length 49136;  
Best Local Similarity 99.4%; Pred. No. 2.4e-174;  
Matches 924; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGAATGCGCCTACAAACACCTGTGGCTCCAGCGACCTCACCTGGCCCCCGAGCGATCAAG 60  
Db 43645 ATGAATGCGCCTACAAACACCTGTGGCTCCAGCGACCTCACCTGGCCCCCGAGCGATCAAG 43704

Qy 61 CTGGGCTTCTACGCTACTTGGGGCTCTGCTGGTGTAGCTGCTGCTCAACAGCGCTG 120  
Db 43705 CTGGGCTTCTACGCTACTTGGGGCTCTGCTGGTGTAGCTGCTGCTCAACAGCGCTG 43764

Qy 121 CGGCTCTGGGTGTTCTGCTGCGCATGCGAGCTGGAGCGGACCGCATCTACATGACC 180  
Db 43765 GCGCTCTGGGTGTTCTGCTGCGCATGCGAGCTGGAGCGGACCGCATCTACATGACC 43824

Qy 181 AACCTGGCGGTGGCGGACCTCTGCTGTGACCTTTGCCCTTGGTGTGCTGCTGCTGCTG 240  
Db 43825 AACCTGGCGGTGGCGGACCTCTGCTGTGACCTTTGCCCTTGGTGTGCTGCTGCTGCTG 43884

Qy 241 CGAGACCTCAGACAGCGCGCTGTCAGCTCTCCAGGCGATCTACCTGACCAACAGG 300  
Db 43885 CGAGACCTCAGACAGCGCGCTGTCAGCTCTCCAGGCGATCTACCTGACCAACAGG 43944

Qy 301 TACATGAGCATCAGCTGGTCCAGCGCATCGCGCTGGACCGCTATGTGGCGTGGCGCAC 360  
Db 43945 TACATGAGCATCAGCTGGTCCAGCGCATCGCGCTGGACCGCTATGTGGCGTGGCGCAC 44004

Qy 361 CCGTGTGCTGCGCGGCTGGTCTCCAGGAGGCTGGCGGCTGGCGGCTGGCGGCTGCTC 420  
Db 44005 CCGTGTGCTGCGCGGCTGGTCTCCAGGAGGCTGGCGGCTGGCGGCTGGCGGCTGCTC 44064

Qy 421 TGGGTGCTGCTCATCGGCTCCCTGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 480  
Db 44065 TGGGTGCTGCTCATCGGCTCCCTGGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 44124

Qy 481 TTCTGCTTCAGGAGCACCGGCGACAATTTCACTCCATGCGGTTCCCGCTGCTGGGATTC 540  
Db 44125 TTCTGCTTCAGGAGCACCGGCGACAATTTCACTCCATGCGGTTCCCGCTGCTGGGATTC 44184

Qy 541 TACTGCCCCCTGGCGGTGGTCTTCTGCTCCCTGAAGGTGGTGAATGCTGCTGCTGCTGCTG 600  
Db 44185 TACTGCCCCCTGGCGGTGGTCTTCTGCTCCCTGAAGGTGGTGAATGCTGCTGCTGCTGCTG 44244

Qy 601 AGGCCACCCAGCGAGTGGGCGAGGAGCGGACCGCCCAAGGCTAAACGATGCTGTGG 660  
Db 44245 AGGCCACCCAGCGAGTGGGCGAGGAGCGGACCGCCCAAGGCTAAACGATGCTGTGG 44304

Qy 661 GCCAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
Db 44305 GCCAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 44364

Qy 721 CTCGAGTGGGCTGGAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
Db 44365 CTCGAGTGGGCTGGAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 44424

Qy 781 ACCAGCAAGCTCTCAGATGCCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840

Db 44425 ACCAGCAAGCTCTCAGATGCCAACACTGCTGCTGGAGCGCATCTGCTACTACTATGCGCC 44484  
Qy 841 AAGGAGTTCCAGGAGGCGTCTGCACTGGCCGCTGGCTCCCGCTGTAAGCCGCCACAAAAGC 900  
Db 44485 AAGGAGTTCCAGGAGGCGTCTGCACTGGCCGCTGGCTCCCGCTGTAAGCCGCCACAAAAGC 44544  
Qy 901 CAGGACTCTCTGCTGGTGAACCTCGCCTAA 930  
Db 44545 CAGGACTCTCTGCTGGTGAACCTCGCCTAA 44574

## RESULT 11

ADF70563  
ID ADF70563 standard; DNA; 1644 BP.  
XX AC ADF70563;  
XX AC  
XX 12-FEB-2004 (first entry)  
XX  
DE Orphan receptor ligand-related human protein gene SeqID186.  
XX  
XX ligand; orphan receptor protein; fusion protein; fluorescent protein;  
KW cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFP;  
KW GFPuv; Enhanced GFP; EGFP; human; gene; ds.  
XX  
XX Homo sapiens.  
XX  
XX WO2003071272-A1.  
XX  
XX 28-AUG-2003.  
XX  
XX 21-FEB-2003; 2003WO-JP001901.  
XX  
XX 22-FEB-2002; 2002JP-00045728.  
PR 23-JUL-2002; 2002JP-00213949.  
PR 11-OCT-2002; 2002JP-00298237.  
XX  
XX (TAKE ) TAKEDA CHEM IND LTD.  
XX  
XX Hinuma S, Fujii R, Ogi K, Komatsu H, Kawamata Y, Hosoya M;  
XX  
XX WPI; 2003-697654/66.  
DR P-FSDB; ADF70461.  
XX  
PT Transformation of cells with a fusion protein of an orphan receptor.  
PT protein with a fluorescent protein useful for identification of ligands  
PT to the orphan receptor.

Example 4; SEQ ID NO 186; 594pp; Japanese.

This invention relates to a novel method of identifying ligands to an  
orphan receptor protein which comprises transforming cells with DNA  
encoding a fusion protein of the orphan receptor with a fluorescent  
protein, so that the fusion protein is expressed in the cells (or cell  
membranes isolated from them) and contacting the cells with the potential  
ligand to be tested. A suitable fluorescent protein for incorporation in  
the fusion protein is green fluorescent protein (GFP), for example GFP-1,  
wild-type GFP, GFPuv or Enhanced GFP (EGFP). The method is useful for the  
identification of ligands binding to an orphan receptor protein.

Sequence 1644 BP; 368 A; 486 C; 431 G; 359 T; 0 U; 0 Other;

Query Match 98.8%; Score 919; DB 10; Length 1644;  
Best Local Similarity 99.5%; Pred. No. 3.2e-174;  
Matches 922; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ATGAATGCGCCTACAAACACCTGTGGTCTCAGCGACCTCACCTGGCCCCCGAGCGATCAAG 60  
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Qy 61 CTGGGCTTCTACGCTACTTGGGGCTCTGCTGGTGTAGGCTGCTGCTCAACAGCGCTG 120  
Db 61 CTGGGCTTCTACGCTACTTGGGGCTCTGCTGGTGTAGGCTGCTGCTCAACAGCGCTG 120











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QY 121 GGGCTCTGGGTCTTCTGTCGCGCATGCGAGTGGACGAGACCCGCACTTACATGACC 180
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QY 839 AAGGAGTTCAGGAGGCGTC 858
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Job time : 630 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 23, 2005, 11:29:51 ; Search time 4375 Seconds  
(without alignments)  
10300.194 Million cell updates/sec

Title: US-10-083-168-84  
Perfect score: 930  
Sequence: 1 atgaatggcaactacaac.....tgctgctgacccctgcctaa 930

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb\_hcg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_ats.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	925.2	99.5	930	6	AX549206
2	925.2	99.5	1299	9	AF027957
3	922	99.1	2270	9	AK172786
4	922	99.1	169391	2	AC111190
5	920.4	99.0	930	9	AY275467
6	920.4	99.0	930	9	CR541765
7	920.4	99.0	1875	6	AR153299
8	920.4	99.0	1875	6	CQ821493
9	920.4	99.0	1875	6	AX677157
10	920.4	99.0	1875	9	AF089087
11	920.4	99.0	49136	6	AR153289
12	920.4	99.0	65674	9	AF158748
13	920.4	99.0	160111	9	AC124862
14	917.2	98.6	3811	6	CQ853452
15	917.2	98.6	3811	9	AK131540
16	915.6	98.5	1043	6	BD221595
17	668	71.8	1332	6	CQ738723
18	549.2	59.1	2538	10	BC027429
19	549.2	59.1	2582	10	AF200349

c	20	549.2	59.1	209326	10	AC110247	AC110247 Mus muscu
c	21	549.2	59.1	242338	10	AC119846	AC119846 Mus muscu
	22	546	58.7	220053	2	AC137209	AC137209 Rattus no
	23	112.8	12.1	1448	9	BC067535	BC067535 Homo sapi
	24	111.6	12.0	1098	6	AR308715	AR308715 Sequence
	25	111.2	12.0	1089	6	CQ734006	CQ734006 Sequence
	26	111.2	12.0	1089	6	AR308557	AR308557 Sequence
	27	111.2	12.0	1365	6	AR270866	AR270866 Sequence
	28	111.2	12.0	1365	6	AX774797	AX774797 Sequence
	29	111.2	12.0	1365	9	HUMGRP4A	L36148 Homo sapien
	30	111.2	12.0	1448	9	BC067536	BC067536 Homo sapi
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	32	111.2	12.0	2696	6	AX952242	AX952242 Sequence
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	43	110	11.8	1098	6	CQ778929	CQ778929 Sequence
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## ALIGNMENTS

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DEFINITION	AX549206					
ACCESSION	AX549206.1	GI:25813914				
VERSION	AX549206.1					
KEYWORDS	Homo sapiens (human)					
SOURCE	Homo sapiens					
ORGANISM	Homo sapiens					
REFERENCE	1	Burmer,G.C., Roush,C.L. and Brown,J.P.				
AUTHORS		Antigenic peptides, such as for G protein-coupled receptors				
TITLE		(GPCRs), antibodies thereto, and systems for identifying such				
JOURNAL		antigenic peptides				
FEATURES		Patent: WO 02061087-A 491 08-AUG-2002;				
source		Lifespan Biosciences, Inc. (US)				
		Location/Qualifiers				
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Matches 927;		Conservative	0;	Mismatches	3;	Indels
					0;	Gaps
					0;	
QY	1	ATGAATGGCAGCTACAAACACCTGTGGCTCCAGCGACCTCAGCTGGCCCCCAGCGATCAAG	60			
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Db	61	CTGGGCTTCTAGCGTCTACTTGGGCGTCTGCTGGTGTAGGCTGCTGTCTCAACGCGCTG	120			
QY	121	GGCTCTCTGGGTGTTCTGCTGCGCATGAGCGAGAGACCGGATCTTACATGACC	180			
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DEFINITION cds.  
ACCESSION AY275467  
VERSION AY275467.1 GI:30526187  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 930)  
Warren,C.N., Aronstam,R.S. and Sharma,S.V.  
Isolation of complete coding sequence for G-protein coupled  
receptor 35 (GPR35)  
JOURNAL Unpublished  
REFERENCE Warren,C.N., Aronstam,R.S. and Sharma,S.V.  
AUTHORS Submitted (11-APR-2003) Guthrie cDNA Resource Center, Guthrie  
TITLE Research Institute, 1 Guthrie Square, Sayre, PA 18840, USA  
JOURNAL Location/Qualifiers  
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ORIGIN  
Query Match 99.0%; Score 920.4; DB 9; Length 930;  
Best Local Similarity 99.4%; Pred. No. 1.5e-135;  
Matches 924; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Qy 1 ATGAATGGCACTTACAAACCTGTGGCTCCAGCGACCTCACCTGGCCGCCCCAGCGATCAAG 60  
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DEFINITION gene GPR35, G protein-coupled receptor 35; complete cds, incl.  
stopcodon.  
ACCESSION CR541765  
VERSION CR541765.1 GI:49456486  
KEYWORDS Full ORF shuttle clone, Gateway(TM), complete cds.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 930)  
Halleck,A., Ebert,L., Moundinya,M., Schick,M., Eisenstein,S.,  
Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W.,  
Korn,B., Zuo,D., Hu,Y. and LaBaer,J.  
Cloning of human full open reading frames in Gateway(TM) system  
entry vector (pDONR201)  
JOURNAL Unpublished

REFERENCE  
AUTHORS

2 (bases 1 to 930)  
Halleck, A., Ebert, L., Moundinya, M., Schick, M., Eisenstein, S.,  
Neubert, P., Kstrang, K., Schattien, R., Shen, B., Henze, S., Mar, W.,  
Korn, B., Zuo, D., Hu, Y., and Labaer, J.

TITLE  
JOURNAL

Direct Submission  
Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer  
Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,  
Germany

## COMMENT

RZPD: RZPD0834D0330D, ORFNO 3528  
www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=RZPD0834D0330D RZPDLIB;  
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.  
834  
www.rzpd.de/products/orfclones/  
www.rzpd.de/products/orfclones/  
Contact: Inge Airlart  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,  
Heubnerweg 6, D-14059 Berlin, Germany  
Tel.: +49 30 32639 100  
Fax: +49 30 32639 111  
www.rzpd.de

This clone is available from RZPD;  
Contact RZPD (customer.service@rzpd.de) for further information.  
Clone name at Harvard Institute of Proteomics  
(www.hip.harvard.edu): FLH131000.01X  
This CDS clone is part of a collection of human full ORF clones  
jointly established and verified by the Harvard Institute of  
Proteomics (HIP) and RZPD.  
This CDS has been cloned incl. stopcodon.  
The CDS has been inserted into pDONR201 via a BP Clonase(TM)  
reaction. Additional sequence has been added in front of the start  
codon: att. .AAAAA GCA GGC TCC ACC (ATG).  
The stopcodon is followed by the 3' att site: GACCCAGCTTTCTT. .att  
The clone is validated by full sequence check.  
Compared to the reference sequence NM\_005301 (GI:33695096) we found  
AA exchange(s) at position (first base of changed triplet):  
880(ser->arg)  
Clone distribution: http://www.rzpd.de/products/orfclones/  
Location/Qualifiers

FEATURES  
source

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## ORIGIN

Query Match 99.0%; Score 920.4; DB 9; Length 930;  
Best Local Similarity 99.4%; Pred. No. 1.5e-135;  
Matches 924; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db

1 ATGAATGGCACTACAAACAGTGTGGCTCCAGGACCTCACCTGGCCCCCAGGATCAAG 60

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RESULT 7
LOCUS AR153299 1875 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 21 from patent US 6235481.
ACCESSION AR153299
VERSION AR153299.1 GI:15120831
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1875)
AUTHORS Horikawa, Y., Oda, N., Hanis, C.L., Bell, G.I. and Cox, N.J.
TITLE Polynucleotides encoding calpain 10
JOURNAL Patent: US 6235481-A 21 22-MAY-2001;
FEATURES Location/Qualifiers
1..1875 source

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Db 1236 GCCAACCTCTGTGTTCTGTTGCTGCTTCTGCTGCCCTGCAGTGGGCTGACAGTGGC 1295  
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LOCUS AX677157 1875 bp DNA linear PAT 27-MAR-2003  
DEFINITION Sequence 350 from Patent WO02103028.  
ACCESSION AX677157  
VERSION AX677157.1 GI:29334605  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Baranova,A.V., Yankovsky,N.K., Korlov,A.P., Lobashev,A.V. and Krukovskaya,L.L.  
TITLE In silico screening for phenotype-associated expressed sequences  
JOURNAL Patent: WO 02103028-A 350 27-DEC-2002;  
Biomedical Center (RU)  
FEATURES  
source location/Qualifiers  
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ORIGIN  
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Best Local Similarity 99.4%; Pred. No. 1.3e-135;  
Matches 924; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy 181 AACCTGGCGGTGGCGACCTCTGCTGCTGTCACCTTCCCTTCTGCTGCTGCTGCTGCTG 240  
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Qy 241 CGAGACACCTCTAGACACGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300  
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Qy 901 CAGGACTCTCTGTGGTGACCTCGCCCTAA 930  
Db 1476 CAGGACTCTCTGTGGTGACCTCGCCCTAA 1505

RESULT 10  
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LOCUS AF089087 1875 bp mRNA linear PRI 03-OCT-2000  
DEFINITION Homo sapiens G protein-coupled receptor mRNA, complete cds.  
ACCESSION AF089087  
VERSION AF089087.1 GI:10503932  
KEYWORDS  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1875)  
AUTHORS Horikawa,Y., Oda,N., Cox,N.J., Li,X., Orho-Melander,M., Hara,M.,  
Hinoio,Y., Lindner,T.H., Mashima,H., Schwarz,P.E., Del  
Bosque-Plata,L., Horikawa,Y., Oda,Y., Yoshiuchi,I., Colilla,S.,  
Polonsky,K.S., Wei,S., Concannon,P., Iwasaki,N., Schulze,J.,  
Baier,L.J., Bogardus,C., Groop,L., Boerwinkle,E., Hanis,C.L. and  
Bell,G.I.

TITLE Genetic variation in the gene encoding calpain-10 is associated  
with type 2 diabetes mellitus  
JOURNAL Nat. Genet. 26 (2), 163-175 (2000)  
MEDLINE 20472315  
PUBMED 11017071  
REFERENCE 2 (bases 1 to 1875)  
AUTHORS Horikawa,Y. and Bell,G.I.  
TITLE Direct Submission  
JOURNAL Submitted (02-SEP-1998) Howard Hughes Medical Institute, The  
University of Chicago, 5841 S. Maryland Avenue, MC1028, Chicago, IL  
60637, USA

location/Qualifiers  
1..1875  
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/mol\_type="mRNA"

FEATURES  
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 QY 901 CAGGACTCTCTGTGCGTGACCTCCGCTAA 930  
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RESULT 13  
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 LOCUS Homo sapiens BAC clone RP11-27M15 DNA linear PRI 15-OCT-2002  
 DEFINITION AC124862 AC080022  
 ACCESSION  
 VERSION  
 AC124862.4 GI:22758809  
 HTG.  
 SOURCE  
 AC124862 Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 160111)  
 Sultato,J.E. and Waterston,R.  
 TITLE Toward a complete human genome sequence  
 JOURNAL Genome Res. 8 (11), 1097-1108 (1998)  
 MEDLINE 99053792  
 PUBMED 9847074

REFERENCE 2 (bases 1 to 160111)  
 AUTHORS Trani,L., Haakenson,W. and Schatzkammer,K.  
 TITLE The sequence of Homo sapiens BAC clone RP11-27M15  
 JOURNAL Unpublished (2001)  
 REFERENCE 3 (bases 1 to 160111)  
 AUTHORS Waterston,R.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (18-JUN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 4 (bases 1 to 160111)  
 AUTHORS Waterston,R.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (08-AUG-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 5 (bases 1 to 160111)  
 AUTHORS Waterston,R.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (08-SEP-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 6 (bases 1 to 160111)  
 AUTHORS Waterston,R.  
 TITLE Direct Submission  
 JOURNAL Submitted (18-SEP-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE 7 (bases 1 to 160111)  
 AUTHORS Waterston,R.  
 TITLE Direct Submission  
 JOURNAL Submitted (15-OCT-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 On Sep 8, 2002 this sequence version replaced gi:22091410.

----- Genome Center  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: http://genome.wustl.edu/gsc  
 Contact: sapiens@wustl.edu  
 ----- Summary Statistics  
 Center project name: H\_NH0027M15  
 Drafting Center: WIBR  
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap

between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

#### MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

#### SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>  
 VECTOR: pBACe3.6

#### NEIGHBORING SEQUENCE INFORMATION:

This sequence is not the entire insert of the clone. This clone is overlapped by AC011298 and AC110619.

A transposon was identified in the finished region of this clone and removed prior to submission. The transposon would insert after base pair 85233 of this sequence.

The region from 21167 to 21405 was derived from a PCR product of project DNA.

The region from 107532 to 107628 was derived from a PCR product of project DNA.

The region from 126169 to 126182 was derived from a PCR product of project DNA.

The region from 126366 to 126648 was derived from a PCR product of project DNA.

Polymorphisms have been identified between AC108015, AC111190 and this sequence.

Data from AC108015 and AC111190 was used to finish this clone.

The sequence of AC080022 has been incorporated into AC124862.

#### FEATURES

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QY 781 ACCAGCAAGCTCTCAGATGCCCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
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RESULT 14  
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LOCUS CQ853452 3811 bp DNA linear PAT 23-AUG-2004  
DEFINITION Sequence 3921 from Patent EP1447413.  
ACCESSION CQ853452  
VERSION CQ853452.1 GI:51509708  
KEYWORDS -  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE AUTHORS  TITLE JOURNAL  FEATURES source  ORIGIN	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.									
	1	Isogai, T., Yamamoto, J., Nishikawa, T., Isono, Y., Sugiyama, T., Otsuki, T., Wakamatsu, A., Ishii, S., Nagai, K. and Irie, R.								
		Full-length human cDNA								
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Db	
2812	TACATGACATCAGCCTGCTCACGCCCATCGCCGTGGACCGCTATGTGCCCGTGGCGCAC 2871
Qy	361 CCGCTGCTGCCCGCGGCTGCGGTCCCGCAGGAGGCTGGCGCCGCTGTGGCGGTCCTC 420
Db	
2872	CCGCTGCTGCCCGCGGCTGCGGTCCCGCAGGAGGCTGGCGCCGCTGTGGCGGTCCTC 2931
Qy	421 TGGGTGCTGGTTCATCGGCTCCCTGCTGGTGGCTCGCTGGCTCCTGGGGATTTCAGGAGGGCGGC 480
Db	
2932	TGGGTGCTGGTTCATCGGCTCCCTGCTGGTGGCTCGCTGGCTCCTGGGGATTTCAGGAGGGCGGT 2991
Qy	481 TTCTGCTTTCAGGAGCACCGGCACAAATTTCAACTCCATCGGTCCCGCTGCTGGGATTTC 540
Db	
2992	TTCTGCTTTCAGGAGCACCGGCACAAATTTCAACTCCATCGGTCCCGCTGCTGGGATTTC 3051
Qy	541 TACCTGCCCCCTGGCGTGGTGGTCTTTCTGCTCCCTGAAGGTGGTGACTGCCCTGGCCCCAG 600
Db	
3052	TACCTGCCCCCTGGCGTGGTGGTCTTTCTGCTCCCTGAAGGTGGTGACTGCCCTGGCCCCAG 3111
Qy	601 AGGCCACCCACCGAGCTGGGGCAGGACAGAGCCACCGCAAGGCTAAACGCATGCTCTGG 660
Db	
3112	AGGCCACCCACCGAGCTGGGGCAGGACAGAGCCACCGCAAGGCTGCCCGCATGGTCTGG 3171
Qy	661 GCCAACCTCCTGGTGTCTGTGTCTGTCTTCTGCCCCCTGCACGTGGGGCTGACAGTGGCG 720
Db	
3172	GCCAACTCCTGGTGTCTGTGTCTGTCTTCTGCCCCCTGCACGTGGGGCTGACAGTGGCG 3231
Qy	721 CTCGCAGTGGGTGGAACGCTGTGCCCTCTCTGGAGAGCATCCGTTCGGCCCCCTGTACATA 780
Db	
3232	CTTGCAGTGGGTGGAACGCTGTGCCCTCTCTGGAGATGATCCGTTCGGCCCCCTGTACATA 3291
Qy	781 ACCAGCAAGCTCTAGATGCCAACTGTGCTGCTGGAGCGGCATCTGCTACTACATGGCC 840
Db	
3292	ACCAGCAAGCTCTAGATGCCAACTGTGCTGCTGGAGCGGCATCTGCTACTACTACATGGCC 3351
Qy	841 AAGGAGTTTCCAGGAGGCGTCTGCACTGGCCGCTGCCCTCCCGTGTAAAGGCCACAAAGC 900
Db	
3352	AAGGAGTTTCCAGGAGGCGTCTGCACTGGCCGCTGCCCTCCCGTGTAAAGGCCACAAAGC 3411
Qy	901 CAGGACTCTCTGTGGTGAACCTCGCCTAA 930
Db	
3412	CAGGACTCTCTGTGGTGAACCTCGCCTAA 3441

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 23, 2005, 11:15:00 ; Search time 17 Seconds  
(without alignments)  
1748.881 Million cell updates/sec

Title: US-10-083-168-16  
Perfect score: 1614  
Sequence: 1 MNGYNTCGSDLTWPPAIAK.....AVAPRAKAKSODSLCVTLA 309

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	401	24.8	370	2 JC5549	heptahelical P2Y5-
2	368.5	22.8	308	2 IS0241	G protein-coupled
3	368.5	22.8	387	2 I8202	G protein-coupled
4	360.5	22.3	344	2 T09508	intron 17 purinerg
5	319	19.8	328	2 I5450	G protein-coupled
6	319	19.8	373	2 A47556	ATP receptor P2u -
7	318	19.7	362	2 S33733	G protein-coupled
8	315.5	19.5	365	2 S68679	G protein-coupled
9	312.5	19.4	364	2 JQ1488	bradykinin B2 rece
10	312.5	19.4	366	1 OORTB2	bradykinin recepto
11	310	19.2	342	2 S13638	platelet-activatin
12	308.5	19.1	375	2 A54946	P-2U nucleotide re
13	305.5	18.9	354	2 IS3033	G protein-coupled
14	305.5	18.9	362	2 A57641	G protein-coupled
15	305	18.9	352	2 S60024	bradykinin B1 rece
16	304	18.8	342	2 A40191	platelet-activatin
17	302.5	18.7	362	2 B57641	G protein-coupled
18	302.5	18.7	373	2 JC4162	P2Y receptor - bov
19	301.5	18.7	362	2 S68207	G protein-coupled
20	298.5	18.5	373	2 JC4737	G protein-coupled
21	293	18.2	341	2 S43252	platelet-activatin
22	291	18.0	328	2 JC4800	P2Y6 receptor - hu
23	289	17.9	363	2 JC2543	angiotensin II rec
24	288.5	17.9	352	2 A43113	chemokine (C-C) re
25	285.5	17.7	361	2 B45680	G protein-coupled
26	283	17.5	341	2 S63666	platelet activatin
27	281.5	17.4	366	2 I49519	bradykinin B2 rece
28	279.5	17.3	363	2 I57955	somatostatin recep
29	279.5	17.3	364	2 JN0763	somatostatin recep

30	278	17.2	363	2 A49092	angiotensin II rec
31	276.5	17.1	361	2 JC5653	G protein-coupled
32	275	17.0	363	2 I48261	angiotensin II rec
33	275	17.0	363	2 I57940	somatostatin recep
34	272.5	16.9	355	2 I49339	macrophage inflam
35	271.5	16.8	420	2 I51667	thrombin receptor
36	271	16.8	354	2 T09353	G protein-coupled
37	269.5	16.7	365	2 S68208	G protein-coupled
38	269	16.7	323	1 Q0BED3	HHRF3 protein - hu
39	268	16.6	418	2 A46226	somatostatin recep
40	266.5	16.5	355	2 JC5067	G protein-coupled
41	263.5	16.3	369	2 JC5068	G protein-coupled
42	262.5	16.3	355	2 A45177	chemokine (C-C) re
43	262.5	16.3	391	2 A41795	somatostatin recep
44	262.5	16.3	391	2 C41795	somatostatin recep
45	262.5	16.3	391	2 A39297	somatostatin recep

ALIGNMENTS

RESULT 1

JC5549  
heptahelical P2Y5-like receptor - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Sep-1997 #sequence\_revision 05-Sep-1997 #text\_change 09-Jul-2004  
C:Accession: JC5549  
R:Janssens, R.; Boeynaems, J.M.; Godart, M.; Communi, D.  
Biochem. Biophys. Res. Commun. 236, 106-112, 1997  
A:Title: Cloning of a human heptahelical receptor closely related to the P2Y5 receptor.  
A:Reference number: JC5549; MUID:97366605; PMID:9223435  
A:Accession: JC5549  
A:Molecule type: DNA  
A:Residues: 1-370 <JAN>  
C:Cross-references: UNIPROT:Q99677; DDBJ:AF005419; NID:g2240034; PIDN:AAB6322.1; PID:g2240034  
C:Superfamily: ATP receptor P2u

Query Match 24.8%; Score 401; DB 2; Length 370;  
Best Local Similarity 34.0%; Pred. No. 2.7e-29;  
Matches 105; Conservative 58; Mismatches 104; Indels 42; Gaps 11;

QY	25	AYLVGLVLLGILLNSLALWFCRCMQWTFRIYNTNLAVADCLLCTLPF-VLHSLR---	81
DB	44	AVYSVVFILGILTNSVSLVFCFRMKRSETAIFTNLAVSLLFVCTLPFKIFYNFNRH	103
QY	82	-DTSPTPCQLSQGIYLTNRYSISLTAIAVDYVAVRHPLRARGLSRPROAAVCAVL	140
DB	104	WPFGDT-LCKISGTAFTNIYGSMLFLTCISVDREPLAIVYPRSTIITRRNSAIVCAGV	162
QY	141	WLVIGSLVARWLLGIOEGGF-----CFR-----STRHFNFSMRPFLLGPLYL	182
DB	163	WILVLSG-----GISASLFTTNVNNATTTCFGLSKRVKTKYLSKITIPIEVVGFI	215
QY	193	PLAVVVFCSLKVVTALAPPTDVCQAEAT-RKAARMWANLLVFVCFPLHVGTLVRL	241
DB	216	PLILNVSCSSVVLRTL--RKPATLSQIGTNKKKVLKMITVHMVAVFVCFVPSVNSVFLYA	273
QY	242	AVGNWAC--ALLETTIRALY-ITSKLSDANCLDAICYVMKAEQFQESALAVAPRAKAH	298
DB	274	LVRSAITNCFERPAKIMYPITLCLATLNCDFEPIFYFTLESFQKSFYI-----NAH	327
QY	299	KSQDSLCVT 307	
DB	328	IRMESLFKT 336	

RESULT 2

IS0241  
G protein-coupled receptor 6H1 - chicken  
N:Alternate names: purinoceptor 6H1  
C:Species: Gallus gallus (chicken)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C:Accession: IS0241; JC4618

R;Kaplan, M.H.; Smith, D.I.; Sundick, R.S.  
 J. Immunol. 151, 628-636, 1993  
 A>Title: Identification of a G protein coupled receptor induced in activated T cells.  
 A:Reference number: 150241; PMID:93329058; PMID:9393036  
 A:Accession: I50241  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-308 <KAP>  
 A:CROSS-references: UNIPROT:P32250; GB:I06109; NID:g304383; PIDN:AAB06587.1; PID:g304384  
 R;Webb, T.E.; Kaplan, M.G.; Barnard, E.A.  
 Biochem. Biophys. Res. Commun. 219, 105-110, 1996  
 A>Title: Identification of 6H1 as a P2Y purinoceptor: P2Y5.  
 A:Reference number: JC4618; MUID:96190677; PMID:8619790  
 A:Accession: JC4618  
 A:Molecule type: mRNA  
 A:Residues: 1-308 <WEB>  
 A:CROSS-references: GB:I06109; NID:g304383; PIDN:AAB06587.1; PID:g304384  
 A:Experimental source: T-cells  
 C:Comment: This receptor plays a role in T-cell activation.  
 C:Genetics:  
 A:Gene: P2Y5  
 C:Superfamily: ATP receptor P2u  
 C:Keywords: G protein-coupled receptor; transmembrane protein  
 F:15-40/Domain: transmembrane #status predicted <TM1>  
 F:51-74/Domain: transmembrane #status predicted <TM2>  
 F:89-109/Domain: transmembrane #status predicted <TM3>  
 F:133-153/Domain: transmembrane #status predicted <TM4>  
 F:177-201/Domain: transmembrane #status predicted <TM5>  
 F:227-248/Domain: transmembrane #status predicted <TM6>  
 F:269-292/Domain: transmembrane #status predicted <TM7>

Query Match 22.8%; Score 368.5; DB 2; Length 308;  
 Best Local Similarity 30.3%; Pred. No. 2.2e-26; Mismatches 102; Indels 43; Gaps 10;  
 Matches 91; Conservative 64

QY 10 SSDLTWPPAIIKLGFGY-AYLGVLVLLGLLNSIALWVFCRMOQWETRIYMTNLAVADLC 68  
 DB 3 SNNCTEDSFKTYLGCVFMSVFLGLIANCAVIFFTLKVKNETTYMLNLAISDLL 62

QY 69 LLCTLPFVLHSLRDTSDTP-----LCQLSQGIYLTNRYSISLVTAIVDRYVAVRHLRA 124  
 DB 63 FVFTLPFRIFYE-VVRNWPFGDVLCKISVTLFVTNMYGSIILFCTISVDRLAIVHPFS 121

QY 125 RGLRSPROAAACAVLWLVVI-GSLVARWLLGIQEGGFCFRST-RHNFSMR-----RP- 176  
 DB 122 KTLRTKRNARIVCAVWITVLAGSTPASF-----FQSTNRQNTEQRTCFENPPE 171

QY 177 -----LLGFYPLAVVFGSLKVTALAQRPPTDVQGAETRAKAAVMWA 221  
 DB 172 STWKTYLSRIVIFIEIVGFPIILNVTCTWVLRTL-NKPLTLRNKLSKKKVKMIFFV 230

QY 222 NLLVFWVCFPLPHVGL---TVRLAVGWNACALLETIRRALYITSKLSDANCCLDICYY 278  
 DB 231 HLVIKFCFVPIVNIILYLSLRTQWNCVSVTVAVRTPVPTLCTAVSNCCFDPPIVYVF 290

RESULT 3  
 169202  
 G protein-coupled receptor HM74 - human  
 C:Species: Homo sapiens (man)  
 C:Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 09-Jul-2004  
 C:Accession: I69202  
 R;Nomura, H.; Nielsen, B.W.; Matsushima, K.  
 Int. Immunol. 5, 1239-1249, 1993  
 A>Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte chem  
 A:Reference number: I54751; MUID:94092629; PMID:7505609  
 A:Accession: I69202  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-387 <RES>  
 A:CROSS-references: UNIPROT:P49019; GB:D10923; NID:g219866; PIDN:BAA01721.1; PID:g219867  
 C:Genetics:  
 A:Gene: HM74

C:Superfamily: G protein-coupled receptor 4

Query Match 22.8%; Score 368.5; DB 2; Length 387;  
 Best Local Similarity 34.3%; Pred. No. 2.8e-26; Mismatches 95; Conservative 48; Mismatches 105; Indels 29; Gaps 11;

QY 27 LGVLLVGLLNSIALWVFCRMOQWETRIYMTNLAVADLCCLCTLPFVL-----HSLR 81  
 DB 34 LGLEFIFGLLNGLAALWIFCFHLKSKSRIFLFLNLAADFLIICLPVMDYVVRSDW 93

QY 82 DTSPTPLCQLSQGIYLTNRYSISLVTAIVDRYVAVRHLRAAGLRSPROAAACAVLW 141  
 DB 94 NFGDIP-CRLVLFNFMNRQSGIIFLTVAVDYRVRVHPHALNKISNWTAAIISCLLW 152

QY 142 VLVIG---SILVARWLLGIQEGGFCFR-STRHNF--NSMRPFLGFLYPLAVVVFCSLK 193  
 DB 153 GITVGLTVHLLKKLL-IQNGPANVCISFSICHTFRWHEAMF-LLEFLLPLGLIILFCSAR 210

QY 194 VVTLAQRPPTDVQGAETRAKAAVMWANLWVFCFLPHVGLTVRLAVGW-----N 246  
 DB 211 IILSLRQR---QMDHAKIKRAITFIMVVAIVFVICFLP---SVVVRIRIFMLLHTSGTQ 264

QY 247 ACALLETIRRALYITSKLSDANCCLDICYYMAKEF 283  
 DB 265 NCEVYRVDLAFFITLSFTYNNMLDPVYVYFSSPSF 301

RESULT 4  
 T09508  
 Intron 17 purinergic receptor P2Y5 - human  
 N:Alternate names: G-protein coupled receptor  
 C:Species: Homo sapiens (man)  
 C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
 C:Accession: T09508  
 R;Bohm, S.K.; Trumpff, A.; Khitin, L.M.; Kong, W.; Payan, D.G.; Bunnett, N.W.  
 submitted to the EMBL Data Library, April 1997  
 A:Description: The human purinergic receptor P2Y5 is encoded in intron 17 of the retinol  
 A:Reference number: Z16705  
 A:Accession: T09508  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-344 <BOH>  
 A:CROSS-references: UNIPROT:P43657; EMBL:AF000546; NID:g2323068; PID:g2323069  
 C:Genetics:  
 A:Map position: 13  
 C:Superfamily: ATP receptor P2u  
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 22.3%; Score 360.5; DB 2; Length 344;  
 Best Local Similarity 29.2%; Pred. No. 1.3e-25; Mismatches 90; Conservative 68; Mismatches 107; Indels 43; Gaps 10;

QY 10 SSDLTWPPAIIKLGFGYAYL-GVLLVGLLNSIALWVFCRMOQWETRIYMTNLAVADLC 68  
 DB 6 SSSHCFYNSFKTYLGCVFMSVFLGLVSNCAVIFICVLKVRNETTYTMINLAMSLL 65

QY 69 LLCTLPFVLHSLRDTSDTP-----LCQLSQGIYLTNRYSISLVTAIVDRYVAVRHLRA 124  
 DB 66 FVFTLPFRIFYE-VVRNWPFGDVLCKISVTLFVTNMYGSIILFCTISVDRLAIVYFPKS 124

QY 125 RGLRSPROAAACAVLWLVVI-GSLVARWLLGIQEGG-----FCFRSTRHNFNSMRFP-- 176  
 DB 125 KTLRTKRNARIVCTGWLTVIGGSAPAVFVQSTHSGQNNASACFEN-----FPEA 175

QY 177 -----LLGFYPLAVVFGSLKVTALAQRPPTDVQGAETRAKAAVMWA 221  
 DB 176 TWKTYLSRIVIFIEIVGFPIILNVTCTWVLRTL-NKPLTLRNKLSKKKVKMIFFV 233

QY 222 NLLVFWVCFPLPHVGL---TVRLAVGWNACALLETIRRALYITSKLSDANCCLDICYY 278  
 DB 234 HLVIKFCFVPIVNIILYLSLRTQWNCVSVTVAVRTPVPTLCTAVSNCCFDPPIVYVF 293

QY 279 MAKEFOEA 286

Qy	2	NGYNTCGSDLTWPPAKLGF-----YAYL-----GVLLVGLGLLNSLALWVCCR	48
Db	9	NSTINGTWEGD-----ELGYKCRFNEDFKYVLLPVSYGVVCLNVLGLNVAIIYFLCR	61
Qy	49	MOQWTETRIYMTNLAVADLCLLCTLPVLHSLRDTSTP-----LCQLSQGIYLTNRVMSI	104
Db	62	LKTNASTTTFWFLAVSDLSYAAASLPLLVYYARGDHPFSTVLKLVFLFYTNLYCSI	121
Qy	105	SLVTAIADRYAVRHLRARGLRSPQAAACAVCLVWLVIIGSLVARWLLGIQSGGFCFR	164
Db	122	LFLTICSVHRCGLVRLPLHSLRMRGARYARRVAAVWVLVL-ACQAPVLYPVITTSVRGTR	180
Qy	165	STRHN-----FNSMRPPLGLFYLPVAVVFCSLKVVTALAQRPD--TDVGOAE	210
Db	181	ITCHDTSARELFSHFVAYSSVMGLLL-FAPVFSVILVCYVLMARRLL-KPAYGTGGGLPR	238
Qy	211	ATRKAAAMWANLLVVFVCELPPLHVGTVRLAVGW--NACALLETIRRALYITSKLSDAN	268
Db	239	AKRKSVRTIALVLAVFALCFPLPHVTRTLVYSFRSLDLSCHTLNAINNAVKITRPLASAN	298
Qy	269	CLDAICYY-----MAKEFQEAASALAVAPRAK	296
Db	299	SCLDPVLYFLAGQLRVRFARDAKPPTEPTSPQAR	333
RESULT 7			
S33733			
G protein-coupled receptor - chicken			
C:Species: Gallus gallus (chicken)			
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004			
C:Accession: S33733			
R:Webb T.E.; Simon. J.; Krishhek, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.H.			
FEBS Lett. 324, 219-225, 1993			
A:Title: Cloning and functional expression of a brain G-protein-coupled ATP re			
A:Reference number: S33733; MUID:93285340; PMID:8508924			
A:Accession: S33733			
A:Status: preliminary			
A:Molecule type: mRNA			
A:Residues: 1-362 <WEB>			
A:Cross-references: UNIPROT:P34996; EMBL:X73268; NID:G395084; PIDN:CAAS1716.1;			
C:Superfamily: ATP receptor P2u			
C:Keywords: G protein-coupled receptor; transmembrane protein			
Query Match 19.7%; Score 318; DB 21; Length 362;			
Best Local Similarity 28.2%; Pred. No. 1.2e-21;			
Matches 96; Conservative 63; Mismatches 134; Indels 48; Gaps 12			
Qy	1	MNGTY-----NTCGSSDLTWPPAKLGF-YAYLGVLLVL-----GLLLNSLALWV	44
Db	10	LNGTQPELLAGGWAAGNATTKCSLT-----KTGFQFYVLPVYILVFTIGFLGNSVALWM	64
Qy	45	PCERMQOWTETRIYMTNLAVADLCCLTLPVLHSLRDTSD---TFLCOLSQGIYLTNR	100
Db	65	FVFHMRPWSGISVYMFNLALADFLYVLTLPALIFYFYFNKTDWIIFGDVWCKLQRFIFHVN	124
Qy	101	YMSISLVTAIADRYAVRHLRARGLRSPQAAACAVCLVWLVIIGSLVARWLL-----GI	156
Db	125	YGSILFTLCISVHRVYTGVPVHPLKSLGRKKGNAYVSSLWALV-VAVIAPILFVSGTV	183
Qy	157	QEGG--FCFSTRHNF-----NSMRPPLGLFYLPVAVVFCSLKVVTALAQRPDPTDVGO	208
Db	184	RNKTIITCYDTADEYLRYSFYVSMCTTFWFCIPFVILGCGVLIKVALIYK---DLDN	240
Qy	209	AEATRKAAAMWANLLVVFVCELPPLHVGTVRLAVGN-----ACALLETIRRALYITSK	263
Db	241	SPLRKSIIYLVIIYLTVFAVSYLEPFWYMKTLNLRARLDFTQPMQCAFNDKYVATYVQVTRG	300
Qy	264	LSDANCLDCAICYYMAKEFOEASALAVAPRAKHSQDSL	304
Db	301	LASLNSCVDPILYFLAGDTFR--RLSRATFKSSRSEPNV	339



A:Residues: 1-366 <MCE>  
A:Cross-references: UNIPROT:P25023; GB:MS9967  
R:Pesquero, J.B.; Lindsey, C.J.; Zeh, K.; Faiva, A.C.M.; Ganten, D.; Bader, M.  
J. Biol. Chem. 269, 26920-26925, 1994  
A:Title: Molecular structure and expression of rat bradykinin B2 receptor gene. Evidence  
A:Reference number: A55079; MUID:95014558; PMID:7929432  
A:Accession: A55079  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-75, 'A', 77-366 <PES>  
A:Cross-references: GB:X80187; GB:X80188; GB:X80189; GB:X80190  
R:Wang, D.; Ma, J.; Chao, L.; Chao, J.  
Biochim. Biophys. Acta 1219, 171-174, 1994  
A:Title: Molecular cloning and sequence analysis of rat bradykinin B(2) receptor gene.  
A:Reference number: S47529; MUID:94368850; PMID:8086459  
A:Accession: S47529  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-366 <WAN>  
A:Cross-references: EMBL:L26173; NID:9476749; PIDN:AAA62492.1; PID:9585244  
C:Comment: this G protein-coupled receptor binds the nonapeptide bradykinin.  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; lipoprotein;  
F:31-48/Domain: transmembrane #status predicted <TM1>  
F:79-96/Domain: transmembrane #status predicted <TM2>  
F:107-126/Domain: transmembrane #status predicted <TM3>  
F:154-170/Domain: transmembrane #status predicted <TM4>  
F:197-215/Domain: transmembrane #status predicted <TM5>  
F:245-261/Domain: transmembrane #status predicted <TM6>  
F:314,182/Binding site: carboxydrate (Asn) (covalent) #status predicted  
F:105-186/Disulfide bonds: #status predicted  
F:326/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 19.4%; Score 312.5; DB 1; Length 366;  
Best Local Similarity 28.1%; Pred. No. 3.8e-21;  
Matches 90; Conservative 54; Mismatches 127; Indels 49; Gaps 9;

QY 2 NGTYNTGSSDLTWPAPKLGFGYVGLVGLLNSLALWVFCRMOQWTTETRIYMTN 61  
DB 14 NGTFSEVNCPTPEWMSWLNIAQPLWVFLAALENIFVLSVFLHKTNCTVABEYILGN 73  
QY 62 LAVADLCLLCTLPFVLSLRDTS---TPLCOLSGIYLTNRYMSISLVAIAVDRYVA 117  
DB 74 LAGADLIACGLPFWAITIANNFDMFGEVLRVNTMYMLYSSICFLMLVSDRYIA 133  
QY 118 VHRPLRARGLRSPROAAVCAVLW--VLVIGS--LVARWLLGIORGCGFCFRSTRN--- 169  
DB 134 LVKTSMGMRGVRWAKLYSLVMSCTLLSSPMLVFRMTKDYREEG-----HNVTAC 186  
QY 170 -----FNSMRFPPLGFLYPLAVVVFCSLKVVTALAQRPPPTDVGQAEATKAAKM 218  
DB 187 VIVPSPRSWEVFTNMLNLVGLPLLSIITFTVRIMQVLRNENMKKFEVQTEKKATVL 246  
QY 219 VVANLLVFVFCPLPLHVG--LTVRLAVG-----WNAALLETIRRALYITSKLS---A 267  
DB 247 VLAVLGLFVLCVFPFQISTFDTLLRLGLVSGCN-----ERAVDITQISSVAYS 298  
QY 268 NCCLDAICVYNAKEFQEAS 287  
DB 299 NSCLNPLVTVVIGKFRKKS 318

RESULT 11  
SI3638  
platelet-activating factor receptor - guinea pig  
C:Species: Cavia porcellus (guinea pig)  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
A:Accession: SI3638  
R:Honda, Z.; Nakamura, M.; Miki, I.; Minami, M.; Watanabe, T.; Seyama, Y.; Okado, H.; To  
Nature 349, 342-346, 1991  
A:Title: Cloning by functional expression of platelet-activating factor receptor from gu  
A:Reference number: SI3638; MUID:91101726; PMID:1846231  
A:Accession: SI3638

A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-342 <HON>  
A:Cross-references: UNIPROT:P21556; GB:X56736; NID:949442; PIDN:CAA40060.1; PID:949443  
A:Note: the species of guinea pig is not identified; in GenBank entry CCDAFREC, release  
C:Superfamily: ATP receptor P2u

Query Match 19.2%; Score 310; DB 2; Length 342;  
Best Local Similarity 28.2%; Pred. No. 6e-21;  
Matches 81; Conservative 58; Mismatches 110; Indels 38; Gaps 9;

QY 29 VLLVGLLLNSLALWVFCRMOQWTTETRIYMTNLAVALDCLCTLP--FVLHSLRDT 83  
DB 24 IIFVGLIANGVVLWVF-ARLYPSKLEIKLFMNLTVDLLFLITLPLWIVVYSNQN 82  
QY 94 SDTP--LCQLSGIYLTNRYMSISLVAIAVDRYVAVRHPLRARGLRSPROAAVCAVLW 141  
DB 83 WFLPKFLCNLAGCLFFINTYCSVFLGVITYNRFOAVKYPKTAQTATTKRGIALSLVW 142  
QY 142 VLVIGSLVARWLLGQEQ-----GGFCFRSTRHNFNSMRPPL-----LGFVPLA 185  
DB 143 VAIVAA--ASYFLVMDSTNVVSNKAGSGNITRCFEHYEKGSKPVLIIHICIVLGFIVFL 200  
QY 186 VVVFCSLKVVTALAQRPPPTDVGQAEATKAAKMVWVWVVFVFCFLPLHVLTVRLAVGM 245  
DB 201 LILFCNLVLIHTLLRQPKVQQRNAEVRRLMMVCTVLAVFVICFVPHHM-----VOLPW 255  
QY 246 NACAL-----LETIRBALYITSKLSDANCCDLAICYIYMAKBFQE 285  
DB 256 TLAEIGMWPSSNHQAINDAHQVTLCLLSTNCVLDPIVFCFLTKKFRK 302

RESULT 12  
AS4946  
P-2U nucleotide receptor - human  
C:Species: Homo sapiens (man)  
C:Date: 11-Nov-1994 #sequence\_revision 11-Nov-1994 #text\_change 17-Mar-1999  
A:Accession: AS4946  
R:Par, C.E.; Sullivan, D.M.; Paradiso, A.M.; Lazarowski, E.R.; Burch, L.H.; Olsen, J.C.  
Proc. Natl. Acad. Sci. U.S.A. 91, 3275-3279, 1994  
A:Title: Cloning and expression of a human P-2U nucleotide receptor, a target for cysti  
A:Reference number: AS4946; MUID:94211846; PMID:8159738  
A:Accession: AS4946  
A:Status: preliminary  
A:Molecule type: mRNA; protein  
A:Residues: 1-375 <PAR>  
A:Cross-references: GB:U07225  
A:Note: parts of this sequence were confirmed by protein sequencing  
C:Genetics:  
A:Gene: GDB:P2RY2; HP2U; P2U  
A:Cross-references: GDB:362713; OMIM:600041  
A:Map position: 11q13.5-11q14.1  
C:Superfamily: ATP receptor P2u  
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 19.1%; Score 308.5; DB 2; Length 375;  
Best Local Similarity 31.7%; Pred. No. 9e-21;  
Matches 89; Conservative 41; Mismatches 104; Indels 47; Gaps 8;

QY 28 GVLLVGLLLNSLALWVFCRMOQWTTETRIYMTNLAVALDCLCTLPFVLHSLRDTSDTP 87  
DB 41 GVVCVLGLCLNAVGLYIFLCRLKTWNASTTYNFHLAVSDALYASLPLVLYYARGDHP 100  
QY 88 ---LCQLSGIYLTNRYMSISLVAIAVDRYVAVRHPLRARGLRSPROAAVCAVLWVL 143  
DB 101 FSTVLCKLVRLFYTNLYCSILFLTCISVHRCLGVLRPLRSURWGRYARRVAGAVWL 160  
QY 144 VIGSLVARWLLGIORGCGFCFRSTRHNFNSMRPPL-----SARGPLTCHDTSAPFLSFRFVAYSSVMLGLLF 180  
DB 161 V-----LACQAPLVYFVT-----SARGPLTCHDTSAPFLSFRFVAYSSVMLGLLF 206  
QY 181 YLPLAVVVFCSLKVVTALAQRPP--TDVGQAEATKAAKMVWVWVVFVFCFLPLHVLGT 238  
DB 181 YLPLAVVVFCSLKVVTALAQRPP--TDVGQAEATKAAKMVWVWVVFVFCFLPLHVLGT 238

Db 207 AVPPFAVLVYVLMARRLL-KPAYGTSGGLPRAKRSVRTIAVLAVFALCFLPFHVRT 265  
QY 239 VRLAVGW--NACALLETRIRALYITSKLSDANCCLDAICY 277  
Db 266 LYSFRLSDLSCHTLNAINMA-YKVTRLASANSCLDPVLIY 305

RESULT 13  
I53033  
G protein-coupled receptor - human  
C:Species: Homo sapiens (man)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I53033  
R:Heiber, M.; Docherty, J.M.; Shah, G.; Nguyen, T.; Cheng, R.; Heng, H.H.Q.; Marchese, R.  
DNA Cell Biol. 14, 25-35, 1995  
A:Title: Isolation of three novel human genes encoding G protein-coupled receptors.  
A:Reference number: I53033; MUID:95134353; PMID:7832990  
A:Accession: I53033  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-354 <RES>  
A:Cross-references: UNIPROT:P46093; GB:L36148; NID:G598152; PIDN:AAA63180.1; PID:G598153  
C:Superfamily: G protein-coupled receptor 4  
C:Keywords: G protein-coupled receptor

Query Match 18.9%; Score 305.5; DB 2; Length 354;  
Best Local Similarity 31.0%; Pred. No. 1.6e-20;  
Matches 93; Conservative 48; Mismatches 118; Indels 41; Gaps 11;

QY 2 NGTYNTC---GSSDLTWPPAIKLGFYAYLVGLVLLVGLLNSLALMWFCRCMQQWETRIY 58  
Db 3 NHTWEGCHVDSRVDLHLPFSL-----YIFVIGV-GLPTNCLALMAAYRQVQORNELGY 55

QY 59 MTNLAVADLCCLCTLP-----FVLHSLRDTSDTFLCOLSQGIYLTNRNYSISLVTAIAVD 114  
Db 56 LNNLSIADLLYICTLPWDYFLHNDNIHGPSCKLGFGFYFTYNIYISIAFLCCISVD 115

QY 115 YVAVRHLPLRARGLSRQAAACAVLWLVIGLSVARWLLGIEGGFCFRST-RHNFSNM 173  
Db 116 YLAVAHPLRFARLRVKTAIVAVSSVWATELGANSAP--LFHDE---LFRDRYNTFCPE 170

QY 174 RPPL-----LGFYLPVAVVFCSLKVVTALAQRPPTDVQGAETRKAARMVW 220  
Db 171 KFPMEGWAMNLYRVFVGFPLFPWALMLLSYRGILRAVRGVSYST---ERQEKAKIKRLAL 227

QY 221 ANLLVAVVFCFLPHVGLTVRLAV---GWNACALLETRIRALYITSKLSDANCCLDAICY 276  
Db 228 SLIAIVLCFAPYHVLLRSALYILGRPWD-CGFEERVFSAHYHSSLAFTSLNCVADPILY 286

RESULT 14  
A57641  
G protein-coupled receptor 4 - human  
C:Species: Homo sapiens (man)  
C:Date: 08-Feb-1996 #sequence\_revision 08-Feb-1996 #text\_change 09-Jul-2004  
C:Accession: A57641  
R:Mahadevan, M.S.; Baird, S.; Bailly, J.E.; Shutler, G.G.; Sabourin, L.A.; Tsilfidis, C.  
Genomics 30, 84-88, 1995  
A:Title: Isolation of a novel G protein-coupled receptor (GPR4) localized to chromosome 4.  
A:Reference number: A57641; MUID:96129306; PMID:8595909  
A:Accession: A57641  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-362 <NAH>  
A:Cross-references: UNIPROT:P46093; GB:U21051; NID:G687793; PIDN:AAA98457.1; PID:G687794  
C:Genetics:  
A:Gene: GDB:GPR4  
A:Cross-references: GDB:371710; OMIM:600551  
A:Map position: 19q13.3-19q13.3  
A:Introns: #status absent  
C:Superfamily: G protein-coupled receptor 4  
C:Keywords: G protein-coupled receptor

Query Match 18.9%; Score 305.5; DB 2; Length 362;  
Best Local Similarity 31.0%; Pred. No. 1.6e-20;  
Matches 93; Conservative 48; Mismatches 118; Indels 41; Gaps 11;

QY 2 NGTYNTC---GSSDLTWPPAIKLGFYAYLVGLVLLVGLLNSLALMWFCRCMQQWETRIY 58  
Db 3 NHTWEGCHVDSRVDLHLPFSL-----YIFVIGV-GLPTNCLALMAAYRQVQORNELGY 55

QY 59 MTNLAVADLCCLCTLP-----FVLHSLRDTSDTFLCOLSQGIYLTNRNYSISLVTAIAVD 114  
Db 56 LNNLSIADLLYICTLPWDYFLHNDNIHGPSCKLGFGFYFTYNIYISIAFLCCISVD 115

QY 115 YVAVRHLPLRARGLSRQAAACAVLWLVIGLSVARWLLGIEGGFCFRST-RHNFSNM 173  
Db 116 YLAVAHPLRFARLRVKTAIVAVSSVWATELGANSAP--LFHDE---LFRDRYNTFCPE 170

QY 174 RPPL-----LGFYLPVAVVFCSLKVVTALAQRPPTDVQGAETRKAARMVW 220  
Db 171 KFPMEGWAMNLYRVFVGFPLFPWALMLLSYRGILRAVRGVSYST---ERQEKAKIKRLAL 227

QY 221 ANLLVAVVFCFLPHVGLTVRLAV---GWNACALLETRIRALYITSKLSDANCCLDAICY 276  
Db 228 SLIAIVLCFAPYHVLLRSALYILGRPWD-CGFEERVFSAHYHSSLAFTSLNCVADPILY 286

RESULT 15  
S60024  
Bradykinin B1 receptor - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 24-Aug-1996 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S60024  
R:MacNeil, T.; Bierilo, K.K.; Menke, J.G.; Hees, J.F.  
Biochim. Biophys. Acta 1264, 223-228, 1995  
A:Title: Cloning and pharmacological characterization of a rabbit bradykinin B(1) receptor.  
A:Reference number: S60024; MUID:96085127; PMID:7495867  
A:Accession: S60024  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-352 <MAC>  
A:Cross-references: UNIPROT:P48748; EMBL:U20507; NID:G1041820; PIDN:AAC48482.1; PID:G1041820  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 18.9%; Score 305; DB 2; Length 352;  
Best Local Similarity 26.6%; Pred. No. 1.8e-20;  
Matches 89; Conservative 62; Mismatches 131; Indels 52; Gaps 10;

QY 7 TCGSSDLTWPPAIKLGFYAYLVGLVLLVGLLNSLALMWFCRCMQQWETRIYMTNLAVAD 66  
Db 24 SCGAPDAWDLHLRL-LPTFIIAIFTGLGNSFVLSFVLLARRRLSVAEYILANLAASD 82

QY 67 LCLLCTLPFVHLSLRDTSDTP-----LCQLSQGIYLTNRNYSISLVTAIAVDYVAVRHPL 122  
Db 83 LVFVLGLFPFAENVRNQDFWPGAAALCRVNGVIRKANLGFISIFLVVAISQDRYSVLVHPM 142

QY 123 RARGLSRQAAACAVLWLVIGLSVARWLLGIEGGFCFRSTR-----167  
Db 143 ASRRGRRRQAQTALLW--IAGGL-----LSTPTFVLSRVRAVPELNVSAICILLP 193

QY 168 ----HNFNSMRPFLGFLYLPVAVVFCSLKVVTAL---AQRPTDVQGAETRKAARMVW 220  
Db 194 HEAWHLRWVNLNLGLLPLAAILFFNCHILASLRRRGVRVPSRCGGPRDKSTA-LIL 252

QY 221 ANLLVAVVFCFLPHVGLTVRL-----AVGWNACALLETRIRALYITSKLSDANCCLDAIC 275  
Db 253 TLVAVSLVCWAPYHFFAFLECLWQVHAIG--CCFWEEFTDLGLQLSNFSAFVNSCLNPVI 310

QY 276 YYVMAKER-----QASALAVAPRAKAKHSQ 301  
Db 311 YVFGRLFTKVKWELCQCQCSRLAPVSSRRKE 344

Search completed: May 23, 2005, 11:30:20

Job time : 19 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 23, 2005, 11:07:54 ; Search time 63 Seconds  
(without alignments)  
1896.968 Million cell updates/sec

Title: US-10-083-168-16  
Perfect score: 1614  
Sequence: 1 MNGTNTCGSSDLTPPAIK.....AVAPRAKHSQSLCVTLA 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1614	100.0	309	3 AAY79576	Aay79576 Human G p
2	1614	100.0	309	5 ABG95159	Abg95159 Human GPC
3	1614	100.0	309	6 ABP82002	Abp82002 Human G p
4	1614	100.0	309	7 ADB67656	Adb67656 Human G p
5	1614	100.0	309	8 ADO29394	Ado29394 Human GPC
6	1614	100.0	309	8 ADO78094	Ado78094 Human GPC
7	1609	99.7	309	5 ABG95172	Abg95172 Human GPC
8	1608	99.6	309	3 AAY69989	Aay69989 Human rec
9	1608	99.6	547	7 ADF70461	Adf70461 Orphan re
10	1606	99.5	309	7 ADF50511	Adf50511 Human GPC
11	1602	99.3	309	3 AAY58645	Aay58645 Human G-p
12	1602	99.3	309	6 ADA84069	Ada84069 Human GPC
13	1602	99.3	394	8 ADO78095	Ado78095 Human GPR
14	1602	99.3	394	8 ADR10454	Adr10454 Human pro
15	1382	85.6	286	8 ADP29765	Adp29765 Human sec
16	1124	69.6	307	8 ADO29395	Ado29395 Mouse GPC
17	402	24.9	370	2 AAW62597	Aaw62597 Human 7-c
18	402	24.9	370	5 ABP61511	Abp61511 Human NF-
19	402	24.9	370	6 ABG73513	Abg73513 Human p2y
20	402	24.9	370	6 ABP18170	Abp18170 Human G p
21	402	24.9	370	7 ADH69286	Adh69286 Human pur
22	402	24.9	370	8 ADF91778	Adf91778 Human p2y
23	402	24.9	370	8 ADO29049	Ado29049 Human nov
24	402	24.9	370	8 ADQ88244	Adq88244 Human 241
25	402	24.9	370	8 ADQ81575	Adq81575 Human 1ys

26	402	24.9	508	7 ADF70491	Adf70491 Orphan re
27	401	24.8	370	7 ADH69285	Adh69285 Human pur
28	401	24.8	370	7 ADF91777	Adf91777 Human p2y
29	397	24.6	370	5 ADO29050	Ado29050 Mouse nov
30	392	24.3	370	5 ABP61510	Abp61510 Human NF-
31	385	23.9	327	8 ADO29415	Ado29415 Mouse GPC
32	376.5	23.3	363	5 AAU77993	Aau77993 Human inf
33	376.5	23.3	363	5 ADJ63782	Adj63782 Human G p
34	376.5	23.3	363	7 ADF28998	Adf28998 Human G p
35	376	23.3	319	2 AAY30313	Aay30313 AnMaid G
36	376	23.3	319	3 AAY79562	Aay79562 Human G p
37	376	23.3	319	8 ADH68205	Adh68205 Human G-p
38	376	23.3	319	8 ADR73578	Adr73578 Human var
39	376	23.3	383	4 ABG23843	Abg23843 Novel hum
40	376	23.3	557	7 ADF70422	Adf70422 Orphan re
41	375.5	23.3	362	6 ABG72358	Abg72358 Human orp
42	375.5	23.3	363	2 AAW94654	Aaw94654 G-protein
43	375.5	23.3	363	4 AAU04379	Aau04379 Human G-p
44	375.5	23.3	363	6 ABG72361	Abg72361 Rabbit or
45	375.5	23.3	363	7 ADC86215	Adc86215 Human GPC

## ALIGNMENTS

RESULT 1  
AAY79576  
ID AAY79576 standard; protein; 309 AA.  
XX AAY79576;  
AC AAY79576;  
XX 15-AUG-2000 (first entry)  
DT 15-AUG-2000 (first entry)  
XX Human G protein coupled receptor GPR35.  
DE Human G protein coupled receptor GPR35.  
XX  
XX GPR35; G protein coupled receptor; human; NIDDM1;  
KW non-insulin-dependent diabetes mellitus; CAPN10 gene; calpain 10;  
KW diagnosis; therapy.  
XX Homo sapiens.  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 174  
FT /note= "encoded by GCG"  
FT Misc-difference 294  
FT /note= "encoded by AGT"  
XX  
XX WO200023603-A2.  
XX  
XX 27-APR-2000.  
PD 27-APR-2000.  
XX  
XX 21-OCT-1999; 99WO-US024890.  
PF 21-OCT-1999; 99WO-US024890.  
XX  
XX 21-OCT-1998; 98US-0105052P.  
PR 13-MAY-1999; 99US-0134175P.  
XX  
XX (ARCH-) ARCH DEV CORP.  
PA (ARCH-) ARCH DEV TEXAS SYSTEM.  
XX  
XX Polonsky KS, Horikawa Y, Oda N, Sreenan S, Zhou Y, Otani K;  
PI Hanis CL, Bell GI, Cox NJ;  
XX  
XX WPI; 2000-339702/29.  
DR N-PSDB; AA27485, AAY79574, AAY79576.  
XX  
XX Method for screening for type 2 diabetes mellitus comprises detecting a  
PT polymorphism in a calpain encoding nucleic acid segment or a protease-  
PT encoding nucleic acid segment.  
XX  
XX Claim 75; Page 237-238; 257pp; English.  
XX  
XX The present sequence is that of the human gene encoding G protein coupled  
CC receptor, GPR35 as deduced from a composite cDNA (see AAA27485). The

CC sequence of GPR35 is similar to that of a putative purinoceptor P2Y9  
 CC (34.1% identity) suggesting that ATP or other nucleotide is its ligand.  
 CC GPR35 mRNA was detected in all adult and foetal tissues examined with  
 CC relatively higher levels in adult lung, small intestine, colon and  
 CC stomach. In these tissues, there are 2 major transcripts of 2.4 and 4.4  
 CC kb, whereas in skeletal muscle there is a single transcript of 9.4 kb.  
 CC The GPR35 gene is located in a 49,136 bp region (see AAA27475) within the  
 CC NIDDM1 region of human chromosome 2. This region also includes the CAPN10  
 CC gene, which encodes a novel calpain-like cysteine protease, designated  
 CC calpain 10. Mutations in the CAPN10 gene are responsible for a  
 CC susceptibility to type 2 diabetes. Claimed methods for screening for a  
 CC propensity for type 2 diabetes mellitus are based on detection of a  
 CC polymorphism in a calpain encoding nucleic acid. Methods are also claimed  
 CC for identifying modulators of calpain activity, and using these  
 CC modulators to treat diabetes, in particular through the regulation of an  
 CC insulin secretory response or insulin mediated glucose transport  
 XX

XX Sequence 309 AA;

Query Match 100.0%; Score 1614; DB 3; Length 309;

Best Local Similarity 100.0%; Pred. No. 2.7e-167;

Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTWPPAIKLGFYAYLVGLVLLGLLNSLALWVFCRCMQQTETRIYMT 60

DB 1 MNGTYNTCGSSDLTWPPAIKLGFYAYLVGLVLLGLLNSLALWVFCRCMQQTETRIYMT 60

QY 61 NLAVADLCCLCTLPFVLSLRDSTPLCQLSQGIYLTNRVMSISLVTAIAVDVYVVRH 120

DB 61 NLAVADLCCLCTLPFVLSLRDSTPLCQLSQGIYLTNRVMSISLVTAIAVDVYVVRH 120

QY 121 PLRAGRLSPRQAAACAVLWLVIGSLVARWLLGIOEGGFCFRSTHNFNSMRPFLG 180

DB 121 PLRAGRLSPRQAAACAVLWLVIGSLVARWLLGIOEGGFCFRSTHNFNSMRPFLG 180

QY 181 YLPLAVVVFCSLKVVYVTAQAQRPPTDVQAEATRKAAARMVWVWVFCFLPHVGLTYR 240

DB 181 YLPLAVVVFCSLKVVYVTAQAQRPPTDVQAEATRKAAARMVWVWVFCFLPHVGLTYR 240

QY 241 LAVGNACALLETIRRALYITSKLSDANCLDAICYVYMAKEFQASALAVAPRAKAHKS 300

DB 241 LAVGNACALLETIRRALYITSKLSDANCLDAICYVYMAKEFQASALAVAPRAKAHKS 300

QY 301 QDSLVCVTLA 309

DB 301 QDSLVCVTLA 309

RESULT 2

ABG95159

ID ABG95159 standard; protein; 309 AA.

AC ABG95159;

DT 04-DEC-2002 (first entry)

DE Human GPCR GPR35.

XX Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy;

KW hypertension; reflux disease; depression, migraine; schizophrenia; ulcer;

KW psychotic disorder; asthma; bronchospasm; anaesthesia;

KW myocardial infarction; MI; stroke; glaucoma; anxiety;

KW prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina;

KW prostatic hypertrophy; receptor.

XX Homo sapiens.

OS

XX WO200268600-A2.

PN

XX 06-SEP-2002.

PD

XX 26-FEB-2002; 2002WO-US005625.

XX

PR 26-FEB-2001; 2001US-0271913P.

XX (AREN-) ARENA PHARM INC.

PA

PI Liaw CW, Chalmers DT, Behan DP, Maciejewski-Lenior D, Leonard JN;

PI Lin I, Ortuno D;

XX WPI; 2002-706980/76.

DR N-PSDB; ABS73345.

XX New human G-protein coupled receptor (GPCR), useful for screening agonist

PT or inverse agonist compounds for treating diseases associated with GPCR.

XX Claim 29; Page 128-130; 201pp; English.

XX The present invention relates to transmembrane receptors, particularly

CC endogenous human G-protein coupled receptors (GPCRs), mutant (non-

CC endogenous) versions of the GPCRs, and the polynucleotide sequences

CC encoding them. The GPCRs are useful for screening agonist or inverse

CC agonist compounds for treating diseases associated with GPCR. Diseases

CC that can be treated with such compounds include allergies, hypertension,

CC reflux disease, depression, migraine, schizophrenia, ulcers, psychotic,

CC disorders, asthma, bronchospasm, anaesthesia, myocardial infarction (MI),

CC stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer,

CC anxiety, prostatic hypertrophy, rhinitis, and angina. The present

CC sequence represents an endogenous human GPCR

XX Sequence 309 AA;

Query Match 100.0%; Score 1614; DB 5; Length 309;

Best Local Similarity 100.0%; Pred. No. 2.7e-167;

Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTWPPAIKLGFYAYLVGLVLLGLLNSLALWVFCRCMQQTETRIYMT 60

DB 1 MNGTYNTCGSSDLTWPPAIKLGFYAYLVGLVLLGLLNSLALWVFCRCMQQTETRIYMT 60

QY 61 NLAVADLCCLCTLPFVLSLRDSTPLCQLSQGIYLTNRVMSISLVTAIAVDVYVVRH 120

DB 61 NLAVADLCCLCTLPFVLSLRDSTPLCQLSQGIYLTNRVMSISLVTAIAVDVYVVRH 120

QY 121 PLRAGRLSPRQAAACAVLWLVIGSLVARWLLGIOEGGFCFRSTHNFNSMRPFLG 180

DB 121 PLRAGRLSPRQAAACAVLWLVIGSLVARWLLGIOEGGFCFRSTHNFNSMRPFLG 180

QY 181 YLPLAVVVFCSLKVVYVTAQAQRPPTDVQAEATRKAAARMVWVWVFCFLPHVGLTYR 240

DB 181 YLPLAVVVFCSLKVVYVTAQAQRPPTDVQAEATRKAAARMVWVWVFCFLPHVGLTYR 240

QY 241 LAVGNACALLETIRRALYITSKLSDANCLDAICYVYMAKEFQASALAVAPRAKAHKS 300

DB 241 LAVGNACALLETIRRALYITSKLSDANCLDAICYVYMAKEFQASALAVAPRAKAHKS 300

QY 301 QDSLVCVTLA 309

DB 301 QDSLVCVTLA 309

RESULT 3

ABP82002

ID ABP82002 standard; protein; 309 AA.

XX AC ABP82002;

XX 04-MAR-2003 (first entry)

DT Human G protein-coupled receptor GPR35 protein SEQ ID NO:492.

XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;

KW G protein-coupled receptor modulator; antibody; immune-related disease;

KW growth-related disease; cell regeneration-related disease; AIDS; cancer;

KW immunological-related cell proliferative disease; autoimmune disease;

KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;

osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma; ulcer.

Homo sapiens.

WO200261087-A2.

08-AUG-2002.

19-DEC-2001; 2001WO-US050107.

19-DEC-2000; 2000US-0257144P.

(LIFE-) LIFESPAN BIOSCIENCES INC.

Burmer GC, Roush CL, Brown JP;

WPI; 2003-046718/04.

N-PSDB; AB242852.

New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or autoimmune diseases.

Disclosure; Fig 1; 523pp; English.

The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell regeneration-related disease, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. AB242523 to AB242859 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention

Sequence 309 AA;

Query Match 100.0%; Score 1614; DB 6; Length 309;  
Best Local Similarity 100.0%; Pred. No. 2.7e-167;  
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTPWPAIKLGFAYLVGLVLLGLLNSLALWVFCRMOQTETRIYMT 60  
DB 1 MNGTYNTCGSSDLTPWPAIKLGFAYLVGLVLLGLLNSLALWVFCRMOQTETRIYMT 60  
QY 61 NLAVADLCLLCTLPFVLSLRDTSPTPLCQLSQGIYLTNRYSISLVTAIAVDYRVAVRH 120  
DB 61 NLAVADLCLLCTLPFVLSLRDTSPTPLCQLSQGIYLTNRYSISLVTAIAVDYRVAVRH 120  
QY 121 PLRARGLSRPROAAAVCAVLVWLVIGSLVARWLLGIQEGGFCFRSTRHNFSNMRPFLG 180

Db 121 PLRARGLSRPROAAAVCAVLVWLVIGSLVARWLLGIQEGGFCFRSTRHNFSNMRPFLG 180  
QY 181 YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKARVMWANLLVVFVCFLEPLHVGLTVR 240  
Db 181 YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATRKARVMWANLLVVFVCFLEPLHVGLTVR 240  
QY 241 LAVGHNACALLETTRALYITSKLSDANCCCLDAICYYYMAKEFOEASALAVAPRAKAKHS 300  
Db 241 LAVGHNACALLETTRALYITSKLSDANCCCLDAICYYYMAKEFOEASALAVAPRAKAKHS 300  
QY 301 QDSLCTVILA 309  
Db 301 QDSLCTVILA 309

RESULT 4

ADB67656

ID ADB67656 standard; protein; 309 AA.

XX ADB67656;

XX 04-DEC-2003 (first entry)

XX Human G protein-coupled receptor 35, SEQ ID 25.

XX Cardiant; Gene therapy; heart failure; human;

KW G protein-coupled receptor 35; receptor.

XX Homo sapiens.

XX WO2003072824-A1.

XX 04-SEP-2003.

XX 27-FEB-2003; 2003WO-JP002228.

XX 28-FEB-2002; 2002JP-00054388.

XX 15-APR-2002; 2002JP-00112228.

XX (SANY ) SANKYO CO LTD.

XX Kitakaze M, Takashima S, Asakura M, Isomura T, Furukawa H;

XX Koishi R, Nakamaru K;

XX WPI; 2003-679959/64.

XX N-PSDB; ADB67672.

XX Predicting pathological conditions in heart failure using marker genes and proteins.

XX Claim 1; Page 111-113; 137pp; Japanese.

XX The present invention relates to a method for predicting pathological conditions in heart failure using expression of one of 17 gene sequences (ADB67663-ADB67678); or protein sequences encoded by the genes (ADB67648-ADB67662). The proteins and genes are useful for diagnosis, treatment and prevention of heart failure.

XX Sequence 309 AA;

Query Match 100.0%; Score 1614; DB 7; Length 309;  
Best Local Similarity 100.0%; Pred. No. 2.7e-167;  
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTPWPAIKLGFAYLVGLVLLGLLNSLALWVFCRMOQTETRIYMT 60  
DB 1 MNGTYNTCGSSDLTPWPAIKLGFAYLVGLVLLGLLNSLALWVFCRMOQTETRIYMT 60  
QY 61 NLAVADLCLLCTLPFVLSLRDTSPTPLCQLSQGIYLTNRYSISLVTAIAVDYRVAVRH 120  
DB 61 NLAVADLCLLCTLPFVLSLRDTSPTPLCQLSQGIYLTNRYSISLVTAIAVDYRVAVRH 120  
QY 121 PLRARGLSRPROAAAVCAVLVWLVIGSLVARWLLGIQEGGFCFRSTRHNFSNMRPFLG 180

Db 121 PLRARGLSRQAAAVCAVLWLVIGSLVARWLLGIQGGFCFRSTRNFNSMRPFLG 180  
QY 181 YLPLAVVFCSLKVVTTALAQRPPTDVQGAETRKAARMWVWVVCFLPLHVLTVR 240  
Db 181 YLPLAVVFCSLKVVTTALAQRPPTDVQGAETRKAARMWVWVVCFLPLHVLTVR 240  
QY 241 LAVGNACALLETRRALTITSLDANCCLDIAICYVMKEFOEASALAVAPRAKHS 300  
Db 241 LAVGNACALLETRRALTITSLDANCCLDIAICYVMKEFOEASALAVAPRAKHS 300  
QY 301 QDSLVCVTLA 309  
Db 301 QDSLVCVTLA 309  
RESULT 5  
ADO29394  
ID ADO29394 standard; protein; 309 AA.  
XX ADO29394;  
AC ADO29394;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Human GPCR GPR35, SEQ ID NO:496.  
XX  
KW G protein-coupled receptor; GPCR; drug screening; diagnosis;  
transgenic mouse; neurological disorder; adrenal gland disorder;  
colon disorder; intestinal disorder; cardiovascular disorder;  
muscular disorder; blood disorder; immune disorder; bone disorder;  
joint disorder; metabolic disorder; nutritive disorder; cancer;  
kidney disorder; liver disorder; lung disorder; breast disorder;  
ovary disorder; uterus disorder; prostate disorder; testis disorder;  
skin disorder; stomach disorder; pancreas disorder; spleen disorder;  
thymus disorder; thyroid disorder; antiparkinsonian; antimanic;  
cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;  
CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;  
virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;  
dermatological; antiulcer; antithyroid; antiallergic; anorectic;  
immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;  
receptor.  
XX  
OS Homo sapiens.  
XX  
XX  
PN WO2004040000-A2.  
XX  
XX 13-MAY-2004.  
XX  
XX 09-SEP-2003; 2003WO-US028226.  
XX  
XX 09-SEP-2002; 2002US-0409303P.  
PR 09-APR-2003; 2003US-0461329P.  
XX  
XX (PRIM-) PRIMAL INC.  
XX  
XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;  
PI Madsen L, McIlwain KL, Pavlova MN, Vassiliatis D, Zeng H;  
XX  
XX WPI; 2004-390329/36.  
DR N-PSDB; ADO29916.  
XX  
XX Novel mammalian G protein coupled receptors, useful for identifying  
PT compounds that modulates diagnosing and treating disease condition  
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina  
PT pectoris, Parkinson's disease.  
XX  
PS Claim 151; SEQ ID NO 496; 542pp; English.  
XX  
CC The invention relates to human and mouse G protein-coupled receptors  
(GPCRs) and nucleic acids encoding them. The invention also relates to  
CC sequences at least 90% identical to the GPCR proteins and nucleic acids  
CC of the invention; methods of treating, preventing or diagnosing diseases  
CC associated with GPCRs of the invention; methods of screening for

CC compounds useful in the treatment of GPCR-related diseases; a transgenic  
CC mouse comprising a GPCR gene of the invention; a mouse comprising a  
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
CC from the transgenic mice; kits comprising several mice, each of which has  
CC a mutation in a different GPCR gene of the invention; and kits comprising  
CC probes which hybridise to GPCR polynucleotides of the invention. The  
CC invention further discloses variants of the GPCR polypeptides and vectors  
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may  
CC be used in the diagnosis, treatment or prevention of a wide variety of  
CC diseases including neurological disorders (e.g., Alzheimer's disease,  
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);  
CC disorders of the adrenal gland; disorders of the colon or intestine  
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel  
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
CC myocardial infarction); muscular disorders; blood disorders (e.g.,  
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or  
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid  
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,  
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related  
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,  
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and  
CC thyroid (e.g., cancers). The present sequence represents a GPCR of the  
CC invention. Note: The full sequence data for this patent did not form part  
CC of the printed specification; those sequences not shown were obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 309 AA;  
Query Match 100.0%; Score 1614; DB 8; Length 309;  
Best Local Similarity 100.0%; Pred. No. 2.7e-167;  
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNGYNTCGSSDLTWPPAIKLGFAVLGVLLVGLLNSLALWVFCRQQWTRITYMT 60  
Db 1 MNGYNTCGSSDLTWPPAIKLGFAVLGVLLVGLLNSLALWVFCRQQWTRITYMT 60  
QY 61 NLAVADLCCLCTLPFVLHSLRDTSTPLCOLSQGIYLTNRVMSISLVTAIAVDVAVVRH 120  
Db 61 NLAVADLCCLCTLPFVLHSLRDTSTPLCOLSQGIYLTNRVMSISLVTAIAVDVAVVRH 120  
QY 121 PLRARGLSRQAAAVCAVLWLVIGSLVARWLLGIQGGFCFRSTRNFNSMRPFLG 180  
Db 121 PLRARGLSRQAAAVCAVLWLVIGSLVARWLLGIQGGFCFRSTRNFNSMRPFLG 180  
QY 181 YLPLAVVFCSLKVVTTALAQRPPTDVQGAETRKAARMWVWVVCFLPLHVLTVR 240  
Db 181 YLPLAVVFCSLKVVTTALAQRPPTDVQGAETRKAARMWVWVVCFLPLHVLTVR 240  
QY 241 LAVGNACALLETRRALTITSLDANCCLDIAICYVMKEFOEASALAVAPRAKHS 300  
Db 241 LAVGNACALLETRRALTITSLDANCCLDIAICYVMKEFOEASALAVAPRAKHS 300  
QY 301 QDSLVCVTLA 309  
Db 301 QDSLVCVTLA-309  
RESULT 6  
ADO78094  
ID ADO78094 standard; protein; 309 AA.  
XX  
XX ADO78094;  
XX  
DT 26-AUG-2004 (first entry)  
XX  
XX Human GPR35.  
XX  
KW tumour-associated antigen; TAG; cancer; lung cancer; breast cancer;  
KW prostate cancer; colon cancer; stomach cancer; pancreatic cancer;  
KW ear cancer; nose cancer; kidney cancer; throat cancer; cervical cancer;  
KW melanoma; tumour; human; GPR35.  
XX

OS Homo sapiens.  
 PN DE10254601-A1.  
 PD 03-JUN-2004.  
 PP 22-NOV-2002; 2002DE-01054601.  
 PR 22-NOV-2002; 2002DE-01054601.  
 PA (GANY-) GANYMED PHARM AG.  
 PI Tuereci O, Sahin U, Koslowski M;  
 XX WPI; 2004-421820/40.  
 DR N-PSDB; ADO78086.  
 XX  
 PT Composition containing inhibitor of expression or activity of specific  
 PT tumor-associated antigens, useful for treating cancers, also related  
 PT compositions for diagnosis and monitoring.  
 XX  
 PS Claim 72; SEQ ID NO 9; 124pp; German.  
 XX  
 CC The invention relates to pharmaceutical compositions that comprise an  
 CC agent that inhibits the expression or activity of a tumour-associated  
 CC antigen (Tag) that is encoded by a nucleic acid. The pharmaceutical  
 CC compositions and related compositions, are used for treatment of diseases  
 CC associated with (abnormal) expression of Tag, specifically cancer e.g. of  
 CC lung, breast, prostate, colon, stomach, pancreas, ear/nose/throat, kidney  
 CC or cervix, also melanoma. Compositions containing Tag, or related nucleic  
 CC acid, antibodies or host cells, are also useful for diagnosis and  
 CC monitoring of tumours. The present sequence represents the amino acid  
 CC sequence of a human GPR35.  
 XX  
 SQ Sequence 309 AA;  
 Query Match 100.0%; Score 1614; DB 8; Length 309;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-167;  
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNGTYNTCGSSDLTPWPPAIKLGFYAYLVGLVGLLLNSLALWVFCRMOQWETRIYMT 60  
 DB 1 MNGTYNTCGSSDLTPWPPAIKLGFYAYLVGLVGLLLNSLALWVFCRMOQWETRIYMT 60  
 QY 61 NLAVADLCCLCTLPVLSLSDTSDTPLCQLSQGIYLTNRYSISLVTAIAVDYVAVRH 120  
 DB 61 NLAVADLCCLCTLPVLSLSDTSDTPLCQLSQGIYLTNRYSISLVTAIAVDYVAVRH 120  
 QY 121 PLRAGLSRPRQAAAVCAVWLVVIGSLVARWLLGIQGGFCFRSTRNFNSMRPPLIGF 180  
 DB 121 PLRAGLSRPRQAAAVCAVWLVVIGSLVARWLLGIQGGFCFRSTRNFNSMRPPLIGF 180  
 QY 181 YLPLAVVVFCSIKVVTALAQRPPTDVGOAEATRKARVMWVNLVVFVCFPLPHVGLTVR 240  
 DB 181 YLPLAVVVFCSIKVVTALAQRPPTDVGOAEATRKARVMWVNLVVFVCFPLPHVGLTVR 240  
 QY 241 LAVGNACALLETIRRALYITSKLSDANCCCLDAICYYYWAKEFOEASALAVAPRAKHS 300  
 DB 241 LAVGNACALLETIRRALYITSKLSDANCCCLDAICYYYWAKEFOEASALAVAPRAKHS 300  
 QY 301 QDSLCTVTLA 309  
 DB 301 QDSLCTVTLA 309  
 RESULT 7  
 ID ABG95172  
 XX ABG95172 standard; protein; 309 AA.  
 AC ABG95172;  
 XX  
 DT 04-DEC-2002 (first entry)  
 XX

DE Human GPCR GPR35 mutant A216K.  
 XX  
 KW Human; transmembrane receptor; G-protein coupled receptor; GPCR; allergy;  
 KW hypertension; reflux disease; depression; migraine; schizophrenia; ulcer;  
 KW psychotic disorder; asthma; bronchospasm; anaesthesia;  
 KW myocardial infarction; MI; stroke; glaucoma; anxiety;  
 KW prostatic hyperplasia; epilepsy; prostate cancer; rhinitis; angina;  
 KW prostatic hypertrophy; receptor; mutant; muten.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200268600-A2.  
 XX  
 PD 06-SEP-2002.  
 XX  
 PF 26-FEB-2002; 2002WO-US005625.  
 XX  
 PR 26-FEB-2001; 2001US-0271913P.  
 XX  
 PA (AREN-) ARENA PHARM INC.  
 XX  
 PI Liaw CW, Chalmers DT, Behan DP, Maciejewski-Lenior D, Leonard JN;  
 PI Lin I, Ortuno D;  
 XX  
 DR WPI; 2002-706980/76.  
 XX  
 DR N-PSDB; ABS73401.  
 XX  
 PT New human G-protein coupled receptor (GPCR), useful for screening agonist.  
 PT or inverse agonist compounds for treating diseases associated with GPCR.  
 XX  
 PS Example 2; Page 189-190; 201pp; English.  
 XX  
 CC The present invention relates to transmembrane receptors, particularly  
 CC endogenous human G-protein coupled receptors (GPCRs), mutant (non-  
 CC endogenous) versions of the GPCRs, and the polynucleotide sequences  
 CC encoding them. The GPCRs are useful for screening agonist or inverse  
 CC agonist compounds for treating diseases associated with GPCR. Diseases  
 CC that can be treated with such compounds include allergies, hypertension,  
 CC reflux disease, depression, migraine, schizophrenia, ulcers, psychotic  
 CC disorders, asthma, bronchospasm, anaesthesia, myocardial infarction (MI),  
 CC stroke, glaucoma, prostatic hyperplasia, epilepsy, prostate cancer,  
 CC anxiety, prostatic hypertrophy, rhinitis, and angina. The present  
 CC sequence represents a mutant human GPCR  
 XX  
 SQ Sequence 309 AA;  
 Query Match 99.7%; Score 1609; DB 5; Length 309;  
 Best Local Similarity 99.7%; Pred. No. 9.4e-167;  
 Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MNGTYNTCGSSDLTPWPPAIKLGFYAYLVGLVGLLLNSLALWVFCRMOQWETRIYMT 60  
 DB 1 MNGTYNTCGSSDLTPWPPAIKLGFYAYLVGLVGLLLNSLALWVFCRMOQWETRIYMT 60  
 QY 61 NLAVADLCCLCTLPVLSLSDTSDTPLCQLSQGIYLTNRYSISLVTAIAVDYVAVRH 120  
 DB 61 NLAVADLCCLCTLPVLSLSDTSDTPLCQLSQGIYLTNRYSISLVTAIAVDYVAVRH 120  
 QY 121 PLRAGLSRPRQAAAVCAVWLVVIGSLVARWLLGIQGGFCFRSTRNFNSMRPPLIGF 180  
 DB 121 PLRAGLSRPRQAAAVCAVWLVVIGSLVARWLLGIQGGFCFRSTRNFNSMRPPLIGF 180  
 QY 181 YLPLAVVVFCSIKVVTALAQRPPTDVGOAEATRKARVMWVNLVVFVCFPLPHVGLTVR 240  
 DB 181 YLPLAVVVFCSIKVVTALAQRPPTDVGOAEATRKARVMWVNLVVFVCFPLPHVGLTVR 240  
 QY 241 LAVGNACALLETIRRALYITSKLSDANCCCLDAICYYYWAKEFOEASALAVAPRAKHS 300  
 DB 241 LAVGNACALLETIRRALYITSKLSDANCCCLDAICYYYWAKEFOEASALAVAPRAKHS 300  
 QY 301 QDSLCTVTLA 309  
 DB 301 QDSLCTVTLA 309

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Db      301 QDSLCTLA 309
RESULT 8
ID      AAY69989 standard; protein; 309 AA.
XX      AC      AAY69989;
XX      DT      31-MAY-2000 (first entry)
XX      DE      Human receptor-associated protein from Incyte clone 3083742.
XX      KW      Human receptor-associated protein; HRAP; Incyte clone 3083742;
KW      cytostatic; immunomodulatory; antiinflammatory; cardiant; antianaemic;
KW      antiarteriosclerotic; hepatotropic; antiarthritic antirheumatic;
KW      antiasthmatic; osteopathic; antiallergic; antidiabetic; dermatological;
KW      neuroprotective; diagnosis; treatment; prevention; reproductive disorder;
KW      cardiovascular; cell proliferative; autoimmune; inflammatory; allergy;
KW      gastrointestinal; atherosclerosis; cirrhosis; leukaemia; cancer; AIDS;
KW      arthritis; anaemia; asthma; dermatitis; diabetes; osteoporosis;
KW      multiple sclerosis; irritable bowel syndrome.
XX      OS      Homo sapiens.
XX      FH      Key      Location/Qualifiers
FT      Modified-site 2 /note= "Potential N-glycosylation site"
FT      Modified-site 79 /note= "Potential phosphorylation site"
FT      Modified-site 98 /note= "Potential phosphorylation site"
FT      Region 102..118
FT      /label= Signature_sequence
FT      /note= "G-protein coupled receptor"
FT      Modified-site 129 /note= "Potential phosphorylation site"
FT      Modified-site 165 /note= "Potential phosphorylation site"
FT      Modified-site 191 /note= "Potential phosphorylation site"
FT      Modified-site 212 /note= "Potential phosphorylation site"
FT      Modified-site 238 /note= "Potential phosphorylation site"
FT      Modified-site 253 /note= "Potential phosphorylation site"
FT      Modified-site 261 /note= "Potential phosphorylation site"
FT      /note= "Potential phosphorylation site"
XX      WO200008155-A2.
XX
XX      PD      17-FEB-2000.
XX
XX      PF      06-AUG-1999; 99WO-US017777.
XX
XX      PR      07-AUG-1998; 98US-0160065P.
XX      PR      01-SEP-1998; 98US-0098703P.
XX
XX      (INCY-) INCYTE PHARM INC.
XX
XX      PI      Hillman JL, Yue H, Lal P, Tang YT, Gorgone GA, Guegler KJ;
XX      PI      Corley NC, Baughn MR;
XX
XX      DR      WPI; 2000-205710/18.
XX      DR      N-PSDB; AA250891.
XX
XX      PT      New human receptor-associated proteins (HRAP) useful for the diagnosis,
XX      PT      treatment and prevention of cell proliferative, autoimmune, inflammatory,
XX      PT      reproductive, cardiovascular, and gastrointestinal disorders.
XX
XX      PS      Claim 1; Page 76; 99pp; English.
XX

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CC      The present sequence is human receptor-associated protein (HRAP) from
CC      Incyte clone 3083742 obtained from OVARUN01 cDNA library. This sequence
CC      is expressed in haematopoietic/immune, gastrointestinal and reproductive
CC      tissues. HRAP has cytostatic, immunomodulatory, antiinflammatory,
CC      cardiant, antiarteriosclerotic, hepatotropic, antiarthritic,
CC      antirheumatic, osteopathic, antiallergic, antianaemic, antiasthmatic,
CC      antidiabetic, dermatological and neuroprotective activities. The present
CC      sequence is useful in the diagnosis, treatment and prevention of
CC      disorders associated with HRAP expression, especially cell proliferative,
CC      autoimmune/inflammatory, reproductive, cardiovascular and
CC      gastrointestinal disorders (e.g. atherosclerosis, cirrhosis, leukaemia,
CC      cancer, AIDS, arthritis, allergies, anaemia, asthma, dermatitis,
CC      diabetes, osteoporosis, multiple sclerosis and irritable bowel syndrome)
XX
XX      SQ      Sequence 309 AA;
XX
XX      Query Match      99.6%; Score 1608; DB 3; Length 309;
XX      Best Local Similarity 99.7%; Pred. No. 1.2e-166;
XX      Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX      QY      1 MNGTYNTCGSSDLTPPPAIKLGFAVYLGVLVIGLLNSLALWVFCRMOQTETRIYMT 60
XX      DB      1 MNGTYNTCGSSDLTPPPAIKLGFAVYLGVLVIGLLNSLALWVFCRMOQTETRIYMT 60
XX
XX      QY      61 NLAVADLCLLCTLPFVLSLRDTSPLCQLSQGIYLTNRYSISLVTAIADVVRVVRH 120
XX      DB      61 NLAVADLCLLCTLPFVLSLRDTSPLCQLSQGIYLTNRYSISLVTAIADVVRVVRH 120
XX
XX      QY      121 PLRARGLSRPRQAAAVCAVLWLVIGLSLVARWLLGIQGGFCFRSTRNFNSMRPFLG 180
XX      DB      121 PLRARGLSRPRQAAAVCAVLWLVIGLSLVARWLLGIQGGFCFRSTRNFNSMRPFLG 180
XX
XX      QY      181 YLPLAVVVFCSLKVVTTALAQRPPTDVGQAEATRKARVMWANLLVYVVCFLPLHVGLTVR 240
XX      DB      181 YLPLAVVVFCSLKVVTTALAQRPPTDVGQAEATRKARVMWANLLVYVVCFLPLHVGLTVR 240
XX
XX      QY      241 LAVGNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFOEASALAVAPRAKHS 300
XX      DB      241 LAVGNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFOEASALAVAPRAKHS 300
XX
XX      QY      301 QDSLCTLA 309
XX      DB      301 QDSLCTLA 309
XX
XX      RESULT 9
XX      ID      ADF70461 standard; protein; 547 AA.
XX      AC      ADF70461;
XX      XX      DT      12-FEB-2004 (first entry)
XX      DE      Orphan receptor ligand-related human protein SeqID84.
XX      KW      ligand; orphan receptor protein; fusion protein; fluorescent protein;
XX      KW      cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFP;
XX      KW      GFPuv; Enhanced GFP; EGFP; human.
XX      OS      Homo sapiens.
XX      PN      WO2003071272-A1.
XX      PD      28-AUG-2003.
XX      PF      21-FEB-2003; 2003WO-JP001901.
XX      PR      22-FEB-2002; 2002JP-00045728.
XX      PR      23-JUL-2002; 2002JP-00213949.
XX      PR      11-OCT-2002; 2002JP-00298237.
XX      XX      (TAKE ) TAKEDA CHEM IND LTD.
XX

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PI Hinuma S, Fujii R, Ogi K, Komatsu H, Kawamata Y, Hosoya M;  
 XX WPI; 2003-697654/66.  
 DR N-PSDB; ADF70563.

XX Transformation of cells with a fusion protein of an orphan receptor  
 PT protein with a fluorescent protein useful for identification of ligands  
 PT to the orphan receptor.

XX Disclosure; SEQ ID NO 84; 594bp; Japanese.

XX This invention relates to a novel method of identifying ligands to an  
 CC orphan receptor protein which comprises transforming cells with DNA  
 CC encoding a fusion protein of the orphan receptor with a fluorescent  
 CC protein, so that the fusion protein is expressed in the cells (or cell  
 CC membranes isolated from them) and contacting the cells with the potential  
 CC ligand to be tested. A suitable fluorescent protein for incorporation in  
 CC the fusion protein is green fluorescent protein (GFP), for example GFP-1,  
 CC wild-type GFP, GFPuv or Enhanced GFP (EGFP). The method is useful for the  
 CC identification of ligands binding to an orphan receptor protein.

XX Sequence 547 AA;

Query Match 99.6%; Score 1608; DB 7; Length 547;

Best Local Similarity 99.7%; Pred. No. 2.5e-166;

Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTPWPAIKLGFYALGVLLVGLLLNSLALWVFCRMOQTETRIYMT 60  
 DB 1 MNGTYNTCGSSDLTPWPAIKLGFYALGVLLVGLLLNSLALWVFCRMOQTETRIYMT 60  
 QY 61 NLAVADLCCLCTLPFVLSHSLRDTSTPLCQLSQGIYLTNRYSISLVTAIADRYAVRH 120  
 DB 61 NLAVADLCCLCTLPFVLSHSLRDTSTPLCQLSQGIYLTNRYSISLVTAIADRYAVRH 120  
 QY 121 PLRARGLSRPROAAAVCAVLVVLVGLSVARWLLGIQEGGFCFRSTRHNSMRPPLIGF 180  
 DB 121 PLRARGLSRPROAAAVCAVLVVLVGLSVARWLLGIQEGGFCFRSTRHNSMRPPLIGF 180  
 QY 181 YLPLAVVVFCSLKVVTTALAQRPTDVGQAEATKRAARMVWNLVVFVCFPLHVLTVR 240  
 DB 181 YLPLAVVVFCSLKVVTTALAQRPTDVGQAEATKRAARMVWNLVVFVCFPLHVLTVR 240  
 QY 241 LAVGNACALLETTIRRALYITSKLSDANCCCLDAICYYYMAKEFQASALAVAPRAKHS 300  
 DB 241 LAVGNACALLETTIRRALYITSKLSDANCCCLDAICYYYMAKEFQASALAVAPRAKHS 300  
 QY 301 QDSLVCVTILA 309  
 DB 301 QDSLVCVTILA 309

RESULT 10

ADFS0511

ID ADFS0511 standard; protein; 309 AA.

XX ADFS0511;

XX 12-FEB-2004 (first entry)

DE Human GPCR GPR35 D113A mutein (SeqID 191).

DE mutant; mutein; transformation; endocrine cell line;

DE expression cloning system; bioactive peptide; GPCR ligand; human.

XX Synthetic.

OS Homo sapiens.

XX Key

XX Location/Qualifiers

FT Misc-difference 113

FT /note= "wild type Asp substituted by Ala"

XX WO2003087366-A1.

XX 23-OCT-2003.

XX 16-APR-2003; 2003WO-JP004840.

XX 16-APR-2002; 2002JP-00113030.

XX (KYOW ) KYOWA HAKKO KOGYO KK.

XX Sasaki K, Miura K, Saeki S, Yoshizawa M, Kishimoto K, Kunitomo H;

XX Nishi T, Obinata M;

XX WPI; 2003-833737/77.

XX Endocrine cell lines originated from mammalian hypothalamus and

XX pancreatic islet, applicable in expression cloning systems of bioactive

XX peptide precursor genes, and in screening G protein-coupled receptor

XX ligands.

XX Example 24; SEQ ID NO 191; 316pp; Japanese.

XX This invention relates to a novel method for obtaining a DNA that encodes

XX a peptide acting as agonist, antagonist or inverse agonist on a target

XX receptor. Specifically, it comprises transformation of endocrine cell

XX lines originating from mammalian hypothalamus and pancreatic islets,

XX culturing the transformants and contacting with cells expressing the

XX target receptor. The identification of those cells with a response

XX reaction can be used for selecting a transformant cell line with the

XX appropriate target activity that is expressing the novel transformed DNA.

XX Accordingly, the present invention describes novel cell lines that are

XX applicable in expression cloning systems of bioactive peptide precursor

XX genes, and in screening GPCR ligands for use as drugs including agonists,

XX antagonists and inverse agonists i.e. activators and inhibitors. Such

XX cell lines can provide a highly sensitive and convenient GPCR ligand

XX assay system. This polypeptide sequence is the human GPCR GPR35 D113A

XX mutein of the invention.

XX Sequence 309 AA;

Query Match 99.5%; Score 1606; DB 7; Length 309;

Best Local Similarity 99.7%; Pred. No. 2e-166;

Matches 308; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTPWPAIKLGFYALGVLLVGLLLNSLALWVFCRMOQTETRIYMT 60  
 DB 1 MNGTYNTCGSSDLTPWPAIKLGFYALGVLLVGLLLNSLALWVFCRMOQTETRIYMT 60  
 QY 61 NLAVADLCCLCTLPFVLSHSLRDTSTPLCQLSQGIYLTNRYSISLVTAIADRYAVRH 120  
 DB 61 NLAVADLCCLCTLPFVLSHSLRDTSTPLCQLSQGIYLTNRYSISLVTAIADRYAVRH 120  
 QY 121 PLRARGLSRPROAAAVCAVLVVLVGLSVARWLLGIQEGGFCFRSTRHNSMRPPLIGF 180  
 DB 121 PLRARGLSRPROAAAVCAVLVVLVGLSVARWLLGIQEGGFCFRSTRHNSMRPPLIGF 180  
 QY 181 YLPLAVVVFCSLKVVTTALAQRPTDVGQAEATKRAARMVWNLVVFVCFPLHVLTVR 240  
 DB 181 YLPLAVVVFCSLKVVTTALAQRPTDVGQAEATKRAARMVWNLVVFVCFPLHVLTVR 240  
 QY 241 LAVGNACALLETTIRRALYITSKLSDANCCCLDAICYYYMAKEFQASALAVAPRAKHS 300  
 DB 241 LAVGNACALLETTIRRALYITSKLSDANCCCLDAICYYYMAKEFQASALAVAPRAKHS 300  
 QY 301 QDSLVCVTILA 309  
 DB 301 QDSLVCVTILA 309

RESULT 11

AAVS8645

ID AAVS8645 standard; protein; 309 AA.

XX AAVS8645;

AC AAVS8645;



```

XX 11-APR-2000 (first entry)
XX Human G-protein coupled receptor GPR35A.
XX GPR35A; human; G-protein coupled receptor; purinergic;
XX 7-transmembrane receptor; antibiotic; antifungal; antiviral; analgesic;
XX cytotatic; antidiabetic; anorectic; antiasthmatic; antiparkinsonian;
XX hypertensive; hypertensive; osteopathic; antianginal; cardiac;
XX cerebroprotective; antiulcer; antiallergic; antimagraine; antienetic;
XX tranquilizer; antidepressant; neuroleptic; nootropic; anticonvulsant;
XX therapy; diagnosis; vaccine.
XX Homo sapiens.
XX ADAB4069
XX ID ADAB4069 standard; protein; 309 AA.
XX AC ADAB4069;
XX DT 20-NOV-2003 (first entry)
XX DE Human GPR35 protein.
XX KW human; marker; expressed sequence tag; EST; arabidopsis; tumour;
XX stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;
XX KW vaccine.
XX OS Homo sapiens.
XX XX
XX FN WO2002103028-A2.
XX PD 27-DEC-2002.
XX PF 30-MAY-2002; 2002WO-IB004189.
XX PR 30-MAY-2001; 2001US-0293999P.
XX PR 22-OCT-2001; 2001US-0330457P.
XX PR 19-FEB-2002; 2002US-0357144P.
XX XX
XX PA (BIOM-) BIOMEDICAL CENT.
XX XX
XX PI Baranova AV, Yankovsky NK, Kozlov AP, Lobashev AV, Krukovskaya LL;
XX WPI; 2003-175241/17.
XX DR N-PSDB; ADA84068.
XX XX
XX PT Determining if a nucleic acid is a marker for a phenotype/cell type of
XX interest, by global comparison of expressed sequence tags known to be
XX expressed in the phenotype/cell type with all ESTs expressed in normal
XX tissue.
XX PS Claim 29; Page 448-449; 516pp; English.
XX XX
XX CC The invention relates to a novel method for determining if a nucleic acid
XX is a marker for a predetermined phenotype/cell type of interest from a
XX biological species. The method comprises performing a global comparison
XX of a group of expressed sequence tags (ESTs) known to be expressed in the
XX phenotype/cell type of interest with all ESTs expressed in normal tissue
XX in order to identify ESTs that are preferentially expressed in the
XX phenotype/cell of interest. A method of the invention is useful for
XX determining whether a nucleic acid is a marker for a predetermined
XX phenotype or cell type of interest from a biological species, preferably
XX Arabidopsis or human. The cell type of interest is an abnormal cell such
XX as a tumour cell, and the predetermined phenotype is a stress-induced
XX phenotype such as hyperosmotic stress or high salt conditions. A method
XX of the invention is also useful for determining the progression of colon
XX cancer in a human, for detecting a tumour cell, and for regulating or
XX preventing the growth of a tumour cell. An antibody of the invention is
XX useful for detecting the absence or presence of peptides encoded by
XX tumour-associated markers. A polypeptide of the invention is useful as an
XX immunogen for vaccinating an animal. The present sequence represents a
XX tumour-associated antigen of the invention.
XX SQ Sequence 309 AA;

```

```

XX 11-APR-2000 (first entry)
XX Human G-protein coupled receptor GPR35A.
XX GPR35A; human; G-protein coupled receptor; purinergic;
XX 7-transmembrane receptor; antibiotic; antifungal; antiviral; analgesic;
XX cytotatic; antidiabetic; anorectic; antiasthmatic; antiparkinsonian;
XX hypertensive; hypertensive; osteopathic; antianginal; cardiac;
XX cerebroprotective; antiulcer; antiallergic; antimagraine; antienetic;
XX tranquilizer; antidepressant; neuroleptic; nootropic; anticonvulsant;
XX therapy; diagnosis; vaccine.
XX Homo sapiens.
XX ADAB4069
XX ID ADAB4069 standard; protein; 309 AA.
XX AC ADAB4069;
XX DT 20-NOV-2003 (first entry)
XX DE Human GPR35 protein.
XX KW human; marker; expressed sequence tag; EST; arabidopsis; tumour;
XX stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;
XX KW vaccine.
XX OS Homo sapiens.
XX XX
XX FN WO2002103028-A2.
XX PD 27-DEC-2002.
XX PF 30-MAY-2002; 2002WO-IB004189.
XX PR 30-MAY-2001; 2001US-0293999P.
XX PR 22-OCT-2001; 2001US-0330457P.
XX PR 19-FEB-2002; 2002US-0357144P.
XX XX
XX PA (BIOM-) BIOMEDICAL CENT.
XX XX
XX PI Baranova AV, Yankovsky NK, Kozlov AP, Lobashev AV, Krukovskaya LL;
XX WPI; 2003-175241/17.
XX DR N-PSDB; ADA84068.
XX XX
XX PT Determining if a nucleic acid is a marker for a phenotype/cell type of
XX interest, by global comparison of expressed sequence tags known to be
XX expressed in the phenotype/cell type with all ESTs expressed in normal
XX tissue.
XX PS Claim 29; Page 448-449; 516pp; English.
XX XX
XX CC The invention relates to a novel method for determining if a nucleic acid
XX is a marker for a predetermined phenotype/cell type of interest from a
XX biological species. The method comprises performing a global comparison
XX of a group of expressed sequence tags (ESTs) known to be expressed in the
XX phenotype/cell type of interest with all ESTs expressed in normal tissue
XX in order to identify ESTs that are preferentially expressed in the
XX phenotype/cell of interest. A method of the invention is useful for
XX determining whether a nucleic acid is a marker for a predetermined
XX phenotype or cell type of interest from a biological species, preferably
XX Arabidopsis or human. The cell type of interest is an abnormal cell such
XX as a tumour cell, and the predetermined phenotype is a stress-induced
XX phenotype such as hyperosmotic stress or high salt conditions. A method
XX of the invention is also useful for determining the progression of colon
XX cancer in a human, for detecting a tumour cell, and for regulating or
XX preventing the growth of a tumour cell. An antibody of the invention is
XX useful for detecting the absence or presence of peptides encoded by
XX tumour-associated markers. A polypeptide of the invention is useful as an
XX immunogen for vaccinating an animal. The present sequence represents a
XX tumour-associated antigen of the invention.
XX SQ Sequence 309 AA;

```

```

Query Match 99.3%; Score 1602; DB 3; Length 309;
Best Local Similarity 99.4%; Pred. No. 5.4e-166;
Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
SQ Sequence 309 AA;

```

```

QY 1 MNGTYNTCGSSDLTPPAIKGYPAYLVLLVGLLNSLALWVFCRQMQWTETRIYMT 60
DB 1 MNGTYNTCGSSDLTPPAIKGYPAYLVLLVGLLNSLALWVFCRQMQWTETRIYMT 60
QY 61 NLAVALDCLLCTLPFVHLSDRTSDTFLCQLSQGIYLTNRYSISLTAIVADRYVAVRH 120
DB 61 NLAVALDCLLCTLPFVHLSDRTSDTFLCQLSQGIYLTNRYSISLTAIVADRYVAVRH 120
QY 121 PLRARGLRPRQAAVCAVLWLVIGSLVARWLLGIEGGFCFRSTRHFNFSRPFLLGF 180
DB 121 PLRARGLRPRQAAVCAVLWLVIGSLVARWLLGIEGGFCFRSTRHFNFSRPFLLGF 180
QY 181 YLPLAVVVFCSLKVVTALAQRPPTDVGQAEATKKAARMVMWANLLVFVVCFLPLHVLTVR 240

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Query Match 99.3%; Score 1602; DB 6; Length 309;  
Best Local Similarity 99.4%; Pred. No. 5.4e-166;  
Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTPWPPAIIKLGFYAYLVGLVLLGLLNSLALWVFCRQOQWTEIRIYMT 60  
DB 1 MNGTYNTCGSSDLTPWPPAIIKLGFYAYLVGLVLLGLLNSLALWVFCRQOQWTEIRIYMT 60

QY 61 NLAVADLCLLCTLPFVLSLSDTSDTPLCQSQGIYLTNRYSISLVTAIAVDYVAVRH 120  
DB 61 NLAVADLCLLCTLPFVLSLSDTSDTPLCQSQGIYLTNRYSISLVTAIAVDYVAVRH 120

QY 121 PLRARGLSRPROAAAVCAVLWLVIGSLVARWLLGIOEGGFCFRSTRNFNSMRPILG 180  
DB 121 PLRARGLSRPROAAAVCAVLWLVIGSLVARWLLGIOEGGFCFRSTRNFNSMRPILG 180

QY 181 YLPLAVVVFCSLKVVYTAQAORPPTDVGQAEATRKARMMWANLLVVFVCFPLPHVGLTVR 240  
DB 181 YLPLAVVVFCSLKVVYTAQAORPPTDVGQAEATRKARMMWANLLVVFVCFPLPHVGLTVR 240

QY 241 LAVGNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFOEASALAVAPRAKAHKS 300  
DB 241 LAVGNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFOEASALAVAPRAKAHKS 300

QY 301 QDSLCTVTLA 309  
DB 301 QDSLCTVTLA 309

RESULT 13  
AD078095  
ID AD078095 standard; protein; 394 AA.  
XX AC AD078095;  
XX DT 26-AUG-2004 (first entry)  
XX DE Human GPR35 isoform.  
XX KW tumour-associated antigen; TAG; cancer; lung cancer; breast cancer;  
XX KW prostate cancer; colon cancer; stomach cancer; pancreatic cancer;  
XX KW ear cancer; nose cancer; throat cancer; kidney cancer; cervical cancer;  
XX KW melanoma; tumour; human; GPR35.  
XX OS Homo sapiens.  
XX PN DE10254601-A1.  
XX PD 03-JUN-2004.  
XX PF 22-NOV-2002; 2002DE-01054601.  
XX PR 22-NOV-2002; 2002DE-01054601.  
XX PA (GANY-) GANYMED PHARM AG.  
XX PI Tuereci O, Sahin U, Koslowski M;  
XX WPI; 2004-421820/40.  
XX DR WPI; 2004-421820/40.  
XX PT Composition containing inhibitor of expression or activity of specific  
XX PT tumor-associated antigens, useful for treating cancers, also related  
XX PT compositions for diagnosis and monitoring.  
XX PS Claim 72; SEQ ID NO 10; 124pp; German.  
XX CC The invention relates to pharmaceutical compositions that comprise an  
XX CC agent that inhibits the expression or activity of a tumour-associated  
XX CC antigen (TAG) that is encoded by a nucleic acid. The pharmaceutical  
XX CC compositions and related compositions, are used for treatment of diseases  
XX CC associated with (abnormal) expression of TAG, specifically cancer e.g. of  
XX CC lung, breast, prostate, colon, stomach, pancreas, ear/nose/throat, kidney

CC or cervix, also melanoma. Compositions containing TAG, or related nucleic  
CC acid, antibodies or host cells, are also useful for diagnosis and  
CC monitoring of tumours. The present sequence represents the amino acid  
CC sequence of a human GPR35.  
XX SQ Sequence 394 AA;

Query Match 99.3%; Score 1602; DB 8; Length 394;  
Best Local Similarity 99.4%; Pred. No. 7.4e-166;  
Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNGTYNTCGSSDLTPWPPAIIKLGFYAYLVGLVLLGLLNSLALWVFCRQOQWTEIRIYMT 60  
DB 86 MNGTYNTCGSSDLTPWPPAIIKLGFYAYLVGLVLLGLLNSLALWVFCRQOQWTEIRIYMT 145

QY 61 NLAVADLCLLCTLPFVLSLSDTSDTPLCQSQGIYLTNRYSISLVTAIAVDYVAVRH 120  
DB 146 NLAVADLCLLCTLPFVLSLSDTSDTPLCQSQGIYLTNRYSISLVTAIAVDYVAVRH 205

QY 121 PLRARGLSRPROAAAVCAVLWLVIGSLVARWLLGIOEGGFCFRSTRNFNSMRPILG 180  
DB 206 PLRARGLSRPROAAAVCAVLWLVIGSLVARWLLGIOEGGFCFRSTRNFNSMRPILG 265

QY 181 YLPLAVVVFCSLKVVYTAQAORPPTDVGQAEATRKARMMWANLLVVFVCFPLPHVGLTVR 240  
DB 266 YLPLAVVVFCSLKVVYTAQAORPPTDVGQAEATRKARMMWANLLVVFVCFPLPHVGLTVR 325

QY 241 LAVGNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFOEASALAVAPRAKAHKS 300  
DB 326 LAVGNACALLETIRRALYITSKLSDANCCLDAICYYYMAKEFOEASALAVAPRAKAHKS 385

QY 301 QDSLCTVTLA 309  
DB 386 QDSLCTVTLA 394

RESULT 14  
ADRI0454  
ID ADRI0454 standard; protein; 394 AA.  
XX AC ADRI0454;  
XX DT 04-NOV-2004 (first entry)  
XX DE Human protein useful for treating neurological disease Seq 3960.  
XX KW human; oligo-capping method; diagnostic marker; Gene therapy;  
XX KW osteoporosis; neurological disease; Alzheimer's disease;  
XX KW Parkinson's disease; dementia; short memory; cancer;  
XX KW sense or motor function; emotional reaction; fear response; panic;  
XX KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;  
XX KW tranquiliser.  
XX OS Homo sapiens.  
XX PN EP1447413-A2.  
XX PD 18-AUG-2004.  
XX PF 12-FEB-2004; 2004EP-00003145.  
XX PR 14-FEB-2003; 2003JP-00102207.  
XX PR 09-MAY-2003; 2003JP-00131452.  
XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
XX PI Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;  
XX PI Wakamatsu A, Ishii S, Nagai K, Irie R;  
XX DR WPI; 2004-583265/57.  
XX DR N-PSDB; ADRI0415.  
XX PT New 1995 cDNA, useful for treating osteoporosis, neurological diseases,

PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.  
XX  
PS Claim 1; SEQ ID NO 3960; 2686pp; English.  
XX

CC This invention relates to novel, isolated full length human cDNA  
CC molecules and the encoded proteins thereof. Specifically, it refers to  
CC cDNA clones obtained by an oligo-capping method, where none of these  
CC clones are identical to any known human mRNAs. The present invention  
CC describes an immunoassay to identify agonists and antagonists, as well as  
CC antibodies, antisense molecules and siRNAs that can all be used to bind  
CC to and modulate expression of the cDNA molecules. As such, these  
CC molecules are useful for diagnostic markers or therapeutic targets for  
CC the various diseases or morbid states. In particular, they are useful in  
CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's  
CC disease, Parkinson's disease, dementia, short memory and various cancers,  
CC as well as for maintaining equilibrium of sense or motor function, and  
CC for treating emotional reaction, fear response and panic. Accordingly,  
CC they exhibit osteoprotective, neuroprotective, neurotropic, antiparkinsonian,  
CC cytotactic and tranquiliser activities. This polypeptide is a protein  
CC encoded by a full length human cDNA sequence of the invention. NOTE: This  
CC sequence is not given in the sequence listing of the specification but  
CC can be obtained on CD-ROM from the European Patent Office, Vienna Sub-  
CC office.  
XX  
SQ Sequence 394 AA;

Query Match 99.3%; Score 1602; DB 8; Length 394;  
Best Local Similarity 99.4%; Pred. No. 7.4e-166;  
Matches 307; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MNGTNTCGSSDLTPPPAIKGFYVGLVLLVGLLINSALWVFCRQQQTETRIYMT 60  
DB 86 MNGTNTCGSSDLTPPPAIKGFYVGLVLLVGLLINSALWVFCRQQQTETRIYMT 145  
QY 61 NLAVADLCCLCTLPFVHLSRDTSDTFLCQLSQGIYLTNRYSISLVTIAVDRYVAVRH 120  
DB 146 NLAVADLCCLCTLPFVHLSRDTSDTFLCQLSQGIYLTNRYSISLVTIAVDRYVAVRH 205  
QY 121 PLRARGLRPROAAVCAVLVLTGSLVARMLLGIQGGFCFSTRHNFNSMRPFLG 180  
DB 206 PLRARGLRPROAAVCAVLVLTGSLVARMLLGIQGGFCFSTRHNFNSMAPFLG 265  
QY 181 YLPVAVVFCSLKVTALAQRPPTDVGOAEATRKARMYWANLLVFVVCFLPHVGLTVR 240  
DB 266 YLPVAVVFCSLKVTALAQRPPTDVGOAEATRKARMYWANLLVFVVCFLPHVGLTVR 325  
QY 241 LAVGNACALLETIRALYITSKLSDANCCLDIAICYVMKQFQASALAVAPRAKHS 300  
DB 326 LAVGNACALLEMIRRALYITSKLSDANCCLDIAICYVMKQFQASALAVAPRAKHS 385  
QY 301 QDSLCVTLA 309  
DB 386 QDSLCVTLA 394

RESULT 15  
ADP29765  
ID ADP29765 standard; protein; 286 AA.  
XX  
AC ADP29765;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Human secreted protein SEQ ID #532.  
XX  
KW Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;  
KW cancer; inflammatory; immune; human secreted protein.  
XX  
OS Homo sapiens.  
XX  
PN WO2004035732-A2.  
XX  
PD 29-APR-2004.

XX 28-AUG-2003; 2003WO-US026780.  
PF 29-AUG-2002; 2002US-0406576P.  
XX 29-AUG-2002; 2002US-0406579P.  
PR 29-AUG-2002; 2002US-0406585P.  
PR 29-AUG-2002; 2002US-0406588P.  
PR 29-AUG-2002; 2002US-0406608P.  
PR 29-AUG-2002; 2002US-0406611P.  
PR 29-AUG-2002; 2002US-0406612P.  
PR 29-AUG-2002; 2002US-0406616P.  
PR 29-AUG-2002; 2002US-0406640P.  
PR 29-AUG-2002; 2002US-0406642P.  
PR 29-AUG-2002; 2002US-0406646P.  
PR 29-AUG-2002; 2002US-0406653P.  
PR 29-AUG-2002; 2002US-0406655P.  
PR 29-AUG-2002; 2002US-0406659P.  
PR 17-SEP-2002; 2002US-0406666P.  
PR 17-SEP-2002; 2002US-0410946P.  
PR 17-SEP-2002; 2002US-0410947P.  
PR 17-SEP-2002; 2002US-0410948P.  
PR 17-SEP-2002; 2002US-0410949P.  
PR 17-SEP-2002; 2002US-0410953P.  
PR 17-SEP-2002; 2002US-0410957P.  
PR 17-SEP-2002; 2002US-0410958P.  
PR 17-SEP-2002; 2002US-0410959P.  
PR 17-SEP-2002; 2002US-0410960P.  
PR 17-SEP-2002; 2002US-0410961P.  
PR 17-SEP-2002; 2002US-0410962P.  
PR 17-SEP-2002; 2002US-0411019P.  
PR 17-SEP-2002; 2002US-0411022P.  
PR 17-SEP-2002; 2002US-0411023P.  
PR 17-SEP-2002; 2002US-0411024P.  
PR 17-SEP-2002; 2002US-0411032P.  
PR 17-SEP-2002; 2002US-0411033P.  
PR 17-SEP-2002; 2002US-0411037P.  
PR 17-SEP-2002; 2002US-0411041P.  
PR 17-SEP-2002; 2002US-0411045P.  
PR 17-SEP-2002; 2002US-0411046P.  
PR 17-SEP-2002; 2002US-0411048P.  
PR 17-SEP-2002; 2002US-0411052P.  
PR 17-SEP-2002; 2002US-0411055P.  
PR 17-SEP-2002; 2002US-0411073P.  
PR 17-SEP-2002; 2002US-0411082P.  
PR 17-SEP-2002; 2002US-0411101P.  
PR 17-SEP-2002; 2002US-0411111P.  
PR 18-APR-2003; 2003US-0463700P.  
PR 18-APR-2003; 2003US-0463708P.  
PR 18-APR-2003; 2003US-0463716P.  
PR 18-APR-2003; 2003US-0463732P.  
PR 02-MAY-2003; 2003US-0467199P.  
PR 02-MAY-2003; 2003US-0467201P.  
PR 02-MAY-2003; 2003US-0467203P.  
PR 02-MAY-2003; 2003US-0467230P.  
PR 19-MAY-2003; 2003US-0471306P.  
PR 19-MAY-2003; 2003US-0471336P.  
PR 22-MAY-2003; 2003US-0472420P.  
PR 22-MAY-2003; 2003US-0472430P.  
PR 09-JUN-2003; 2003US-0476609P.  
PR 09-JUN-2003; 2003US-0476641P.  
PR 08-JUL-2003; 2003US-0485218P.  
PR 08-JUL-2003; 2003US-0485223P.  
PR 08-JUL-2003; 2003US-0485242P.  
PR 08-JUL-2003; 2003US-0485325P.  
PR 14-JUL-2003; 2003US-0486446P.  
PR 14-JUL-2003; 2003US-0486480P.  
PR 15-JUL-2003; 2003US-0486891P.  
PR 15-JUL-2003; 2003US-0486960P.  
PR 08-AUG-2003; 2003US-0493341P.  
PR 08-AUG-2003; 2003US-0493370P.  
PR 08-AUG-2003; 2003US-0493573P.  
PR 08-AUG-2003; 2003US-0493577P.  
XX  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.

XX Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;  
PI Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;  
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;  
XX WPI; 2004-348438/32.  
DR  
XX  
XX  
PT New nucleic acid molecule for diagnosing, preventing or treating diseases  
PT such as proliferative (e.g. cancer, inflammatory, immune, metabolic,  
PT genetic, bacterial and viral diseases.  
XX  
XX  
PS Claim 1; SEQ ID NO 1763; 428pp; English.  
XX  
CC The present invention relates to an isolated nucleic acid molecule  
CC encoding a polypeptide which is believed to be cytostatic,  
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The  
CC composition and methods are useful for diagnosing, preventing and  
CC treating diseases such as proliferative (e.g. cancer), inflammatory,  
CC immune, metabolic, genetic, bacterial and viral diseases. The present  
CC sequence represents a human secreted protein. The present sequence is  
CC available on WIPWEB and is not in the specification.  
XX  
SQ Sequence 286 AA;  
  
Query Match 85.6%; Score 1382; DB 8; Length 286;  
Best Local Similarity 99.6%; Pred. No. 5.2e-142;  
Matches 265; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 MNGTYNTCGSSDLTWPPAIKLGFYALGVLLVLGLLNSLALWVCCRQQTETRIYMT 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1 MNGTYNTCGSSDLTWPPAIKLGFYALGVLLVLGLLNSLALWVCCRQQTETRIYMT 60  
  
QY 61 NLAVADLCLLCTLPFVLHSLRDTSTPLCQLSQGIYLTNRNYSISLVTIAVDRYVVRH 120  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||  
61 NLAVADLCLLCTLPFVLHSLRDTSTPLCQLSQGIYLTNRNYSISLVTIAVDRYVVRH 120  
  
QY 121 PLRARGLSRPROAAAVCAVLWLVIGSLVARWLLGIOEGGCFRSTRHFNFSMAFPILGF 180  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||  
121 PLRARGLSRPROAAAVCAVLWLVIGSLVARWLLGIOEGGCFRSTRHFNFSMAFPILGF 180  
  
QY 181 YLPLAVVVFCSLKVVTTALAQRPPTDVGOAETRKAARWVANLLVFVFCFLPHVGLTVR 240  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||  
181 YLPLAVVVFCSLKVVTTALAQRPPTDVGOAETRKAARWVANLLVFVFCFLPHVGLTVR 240  
  
QY 241 LAVGWNACALLETIRRALYITSKLSD 266  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||  
241 LAVGWNACALLETIRRALYITSKLSD 266

Search completed: May 23, 2005, 11:27:38  
Job time : 67 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 23, 2005, 11:25:32 ; Search time 55 Seconds  
(without alignments)  
1879.324 Million cell updates/sec

Title: US-10-083-168-16  
Perfect score: 1614  
Sequence: 1 MNGYNTCGSSDLTPWPAIK.....AVAPRAKAHQSDSLCVTLA 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PTCT\_NEW\_PUB.pep.\*  
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10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*  
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18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
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20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1614	100.0	309	9	US-09-768-877-20
2	1614	100.0	309	14	US-10-225-567A-492
3	1614	100.0	309	17	US-10-696-639-44
4	1602	99.3	309	14	US-10-157-031-351
5	402	24.9	370	10	US-09-964-821B-11
6	402	24.9	370	14	US-10-081-810-44
7	402	24.9	370	14	US-10-225-567A-225
8	402	24.9	370	14	US-10-024-298A-176
9	402	24.9	370	14	US-10-042-211A-176
10	402	24.9	370	14	US-10-268-332-11
11	402	24.9	370	15	US-10-617-217A-176
12	402	24.9	370	17	US-10-753-267-86
13	401	24.8	370	10	US-09-964-821B-10

14	401	24.8	370	14	US-10-268-332-10	Sequence 10, Appl
15	392	24.3	370	14	US-10-024-298A-174	Sequence 174, App
16	392	24.3	370	14	US-10-042-211A-174	Sequence 174, App
17	392	24.3	370	15	US-10-617-217A-174	Sequence 159, App
18	381.5	23.6	363	16	US-10-314-048A-159	Sequence 159, App
19	381.5	23.6	363	16	US-10-897-815-159	Sequence 159, App
20	376.5	23.3	363	10	US-09-930-334-16	Sequence 16, Appl
21	376.5	23.3	363	15	US-10-619-141-16	Sequence 16, Appl
22	376	23.3	319	14	US-10-167-192-1	Sequence 1, Appl
23	376	23.3	319	15	US-10-400-991-4	Sequence 4, Appl
24	375.5	23.3	363	14	US-10-321-807-36	Sequence 36, Appl
25	375.5	23.3	363	15	US-10-295-027-226	Sequence 226, App
26	375.5	23.3	363	15	US-10-292-798-668	Sequence 668, App
27	375.5	23.3	363	16	US-10-321-807-36	Sequence 36, Appl
28	375.5	23.3	363	16	US-10-314-048A-36	Sequence 36, Appl
29	375.5	23.3	363	16	US-10-897-815-36	Sequence 36, Appl
30	375.5	23.3	364	14	US-10-017-161-766	Sequence 766, App
31	375.5	23.3	392	14	US-10-017-161-808	Sequence 808, App
32	371.5	23.0	387	10	US-09-930-334-2	Sequence 2, Appli
33	371.5	23.0	387	15	US-10-619-141-2	Sequence 2, Appli
34	368.5	22.8	308	10	US-09-991-225-7	Sequence 7, Appli
35	368.5	22.8	308	10	US-09-964-821B-12	Sequence 12, Appl
36	368.5	22.8	308	14	US-10-268-332-12	Sequence 12, Appl
37	368.5	22.8	308	15	US-10-369-405-7	Sequence 7, Appli
38	368.5	22.8	339	14	US-10-188-149A-4	Sequence 4, Appli
39	368.5	22.8	387	9	US-09-944-807-21	Sequence 21, Appl
40	368.5	22.8	387	14	US-10-092-135-8	Sequence 8, Appl
41	368.5	22.8	387	14	US-10-251-385-108	Sequence 108, App
42	368.5	22.8	387	14	US-10-251-385-222	Sequence 222, App
43	368.5	22.8	387	14	US-10-240-842-4	Sequence 4, Appli
44	368.5	22.8	387	14	US-10-225-567A-281	Sequence 281, App
45	368.5	22.8	387	14	US-10-296-223-4	Sequence 4, Appli

#### ALIGNMENTS

#### RESULT 1

US-09-768-877-20  
; Sequence 20, Application US/09768877  
; Patent No. US20020150896A1  
; GENERAL INFORMATION:  
; APPLICANT: POLONSKY, KENNETH S.  
; APPLICANT: HORIKAWA, YUKIO  
; APPLICANT: ODA, NAOHISA  
; APPLICANT: COX, NANCY J.  
; APPLICANT: SREENAN, SEAMUS  
; APPLICANT: ZHOU, YUN-PING  
; APPLICANT: OTANI, KENICHI  
; APPLICANT: HANIS, CRAIG L.  
; APPLICANT: BELU, GRAEME I.  
; TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES  
; FILE REFERENCE: ARCD-307  
; CURRENT APPLICATION NUMBER: US/09/768,877  
; CURRENT FILING DATE: 2001-01-23  
; PRIOR APPLICATION NUMBER: 09/422,869  
; PRIOR FILING DATE: 1999-10-21  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Human  
US-09-768-877-20

Query Match 100.0%; Score 1614; DB 9; Length 309;  
Best Local Similarity 100.0%; Pred. No. 8.9e-146;  
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNGYNTCGSSDLTPWPAIKLGFYALGVLLVGLLLSLALWVFCRCMQMOTETRIYMT 60  
DB 1 MNGYNTCGSSDLTPWPAIKLGFYALGVLLVGLLLSLALWVFCRCMQMOTETRIYMT 60

QY 61 NLAVADLCLLCTLPFVHLSLSDTSLPLCQLSGIYLTNRYSISLVTIAVDRYVAVRH 120  
Db |||||  
QY 61 NLAVADLCLLCTLPFVHLSLSDTSLPLCQLSGIYLTNRYSISLVTIAVDRYVAVRH 120  
Db |||||  
QY 121 PLRARGLSRPROAAAACAVLWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPFLG 180  
Db |||||  
QY 121 PLRARGLSRPROAAAACAVLWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPFLG 180  
QY 181 YLPLAVVVFCSLKVVYVFCSLKVVYVFCFLPHVGLTVR 240  
Db |||||  
QY 181 YLPLAVVVFCSLKVVYVFCSLKVVYVFCFLPHVGLTVR 240  
QY 241 LAVGNACALLETIRRALYITSKLSDANCCLDIAICYYWAKEFQESALAVAPRAKAHKS 300  
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QY 301 QDSLVCVTLA 309  
Db |||||  
QY 301 QDSLVCVTLA 309  
Db |||||  
RESULT 2  
US-10-225-567A-492  
; Sequence 492, Application US/10225567A  
; Publication No. US20030113798A1  
; GENERAL INFORMATION:  
; APPLICANT: LifeSpan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burner, Glenna C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/257,144  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 492  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-225-567A-492  
Query Match 100.0%; Score 1614; DB 14; Length 309;  
Best Local Similarity 100.0%; Pred. No. 8.9e-146;  
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNGTYNTCGSSDLTWPPAIKLGFYAYLVGLVLLGLLNSLALWVFCRMOQTETRIYMT 60  
Db |||||  
QY 1 MNGTYNTCGSSDLTWPPAIKLGFYAYLVGLVLLGLLNSLALWVFCRMOQTETRIYMT 60  
Db |||||  
QY 61 NLAVADLCLLCTLPFVHLSLSDTSLPLCQLSGIYLTNRYSISLVTIAVDRYVAVRH 120  
Db |||||  
QY 121 PLRARGLSRPROAAAACAVLWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPFLG 180  
Db |||||  
QY 121 PLRARGLSRPROAAAACAVLWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPFLG 180  
QY 181 YLPLAVVVFCSLKVVYVFCSLKVVYVFCFLPHVGLTVR 240  
Db |||||  
QY 181 YLPLAVVVFCSLKVVYVFCSLKVVYVFCFLPHVGLTVR 240  
QY 241 LAVGNACALLETIRRALYITSKLSDANCCLDIAICYYWAKEFQESALAVAPRAKAHKS 300  
Db |||||  
QY 301 QDSLVCVTLA 309  
Db |||||  
QY 301 QDSLVCVTLA 309  
Db |||||

RESULT 3  
US-10-696-639-44  
; Sequence 44, Application US/10696639  
; Publication No. US20050037439A1  
; GENERAL INFORMATION:  
; APPLICANT: Pharmacia Corporation  
; APPLICANT: Bourner, Maureen J.  
; TITLE OF INVENTION: DIFFERENTIALLY EXPRESSED GENES INVOLVED IN CANCER, THE  
; TITLE OF INVENTION: POLYPEPTIDES ENCODED THEREBY, AND METHODS OF USING THE SAME  
; FILE REFERENCE: 01040/1  
; CURRENT APPLICATION NUMBER: US/10/696,639  
; CURRENT FILING DATE: 2003-10-29  
; PRIOR APPLICATION NUMBER: 60/422,176  
; PRIOR FILING DATE: 2002-10-29  
; NUMBER OF SEQ ID NOS: 3114  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 44  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-696-639-44  
Query Match 100.0%; Score 1614; DB 17; Length 309;  
Best Local Similarity 100.0%; Pred. No. 8.9e-146;  
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNGTYNTCGSSDLTWPPAIKLGFYAYLVGLVLLGLLNSLALWVFCRMOQTETRIYMT 60  
Db |||||  
QY 1 MNGTYNTCGSSDLTWPPAIKLGFYAYLVGLVLLGLLNSLALWVFCRMOQTETRIYMT 60  
Db |||||  
QY 61 NLAVADLCLLCTLPFVHLSLSDTSLPLCQLSGIYLTNRYSISLVTIAVDRYVAVRH 120  
Db |||||  
QY 61 NLAVADLCLLCTLPFVHLSLSDTSLPLCQLSGIYLTNRYSISLVTIAVDRYVAVRH 120  
QY 121 PLRARGLSRPROAAAACAVLWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPFLG 180  
Db |||||  
QY 121 PLRARGLSRPROAAAACAVLWLVIGSLVARWLLGIQEGGFCFRSTRHNFNSMRPFLG 180  
QY 181 YLPLAVVVFCSLKVVYVFCSLKVVYVFCFLPHVGLTVR 240  
Db |||||  
QY 181 YLPLAVVVFCSLKVVYVFCSLKVVYVFCFLPHVGLTVR 240  
QY 241 LAVGNACALLETIRRALYITSKLSDANCCLDIAICYYWAKEFQESALAVAPRAKAHKS 300  
Db |||||  
QY 301 QDSLVCVTLA 309  
Db |||||  
QY 301 QDSLVCVTLA 309  
Db |||||  
RESULT 4  
US-10-157-031-351  
; Sequence 351, Application US/10157031  
; Publication No. US20030108890A1  
; GENERAL INFORMATION:  
; APPLICANT: Baranova, A. V.  
; APPLICANT: Yankovsky, N. K.  
; APPLICANT: Kozlov, A. P.  
; APPLICANT: Lobashev, A. V.  
; APPLICANT: Krukavskaya, L. L.  
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences  
; FILE REFERENCE: 2760-103  
; CURRENT APPLICATION NUMBER: US/10/157,031  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 415  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 351  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-157-031-351



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US-10-225-567A-225
; Sequence 225, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 225
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-225

Query Match      24.9%; Score 402; DB 14; Length 370;
Best Local Similarity 34.1%; Pred. No. 6.3e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

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DB      44  AVYSVVFIILGLITNSVSLFVFCFRMKRSETAIFTNLAVSDLLFVCTLPFKIFYNFNRH 103
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY      82  -DTSDTPLCOLSGIYLTNRYSISLVTAIADRVYAVRHPLRAGRLSPROAAVCAVL 140
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB      104  WPFQDT-LCKISGTAFLTNIGSMFLTCISVDRFLAIYVPPRSRTIRTRNSAIVCAGV 162
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY      141  WVLVIGSLVARWLLGIQE-----GGFCFRSTRHNFNSMR--FPLLGFLPLAVVVF 189
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB      163  WILVLSGGISASLFTSTNNVNTTTCFEGFSKRVKTKITIFIEVVGFIPLILNVS 222
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY      190  CSLKVVTALAQRPTDVGQAEAT-RKAARMVWALLVVFVCFPLHLVGLTVRLAVGWNA 248
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB      223  CSSVVLRTL--RKPAATLSQIGTNKKKVLKMITVHMAVVFVCFVPYNSVLFYALVRSQAI 280
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY      249  --ALLETIRRALY-ITSKLSDANCCLDAICYYYMAKEQESALAVAPRAKAHKSODSLC 305
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB      281  TNCFLERFAKIMYPITLCLATLNCPCDPFIYFTLESFQKSFYI-----NAHIRMESLF 334
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY      306  VT 307
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DB      335  KT 336

RESULT 8
US-10-024-298A-176
; Sequence 176, Application US/10024298A
; Publication No. US20030143540A1
; GENERAL INFORMATION:
; APPLICANT: ASAHI KASEI KABUSHIKI KAISHA
; APPLICANT: AKIO MATSUDA
; APPLICANT: Goichi HONDA
; APPLICANT: Shuji MURAMATSU
; APPLICANT: Yukiko NAGANO
; TITLE OF INVENTION: NF-K B Activating Gene
; FILE REFERENCE: 1254-0191P
; CURRENT APPLICATION NUMBER: US/10/024,298A
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/314,385
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/278,641
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP254018/2001
; PRIOR FILING DATE: 2001-08-24

US-10-042-211A-176
; Sequence 176, Application US/10042211A
; Publication No. US20030170719A1
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Akio et al.
; TITLE OF INVENTION: NFkB Activating Gene
; FILE REFERENCE: 1254-0192P
; CURRENT APPLICATION NUMBER: US/10/042,211A
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: JP 2000-402288
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 2001-088912
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-254018
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/278,640
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/314,385
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-211A-176

Query Match      24.9%; Score 402; DB 14; Length 370;
Best Local Similarity 34.1%; Pred. No. 6.3e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;
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; PRIOR APPLICATION NUMBER: JP0088912/2001
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP402288/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-298A-176

Query Match      24.9%; Score 402; DB 14; Length 370;
Best Local Similarity 34.1%; Pred. No. 6.3e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY      25  AYLGVLVLLGILLNSLALWFCRMOQWETRIYMTNLAVALDCLLCTLPF-VLHSLR-- 81
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB      44  AVYSVVFIILGLITNSVSLFVFCFRMKRSETAIFTNLAVSDLLFVCTLPFKIFYNFNRH 103
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY      82  -DTSDTPLCOLSGIYLTNRYSISLVTAIADRVYAVRHPLRAGRLSPROAAVCAVL 140
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB      104  WPFQDT-LCKISGTAFLTNIGSMFLTCISVDRFLAIYVPPRSRTIRTRNSAIVCAGV 162
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY      141  WVLVIGSLVARWLLGIQE-----GGFCFRSTRHNFNSMR--FPLLGFLPLAVVVF 189
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB      163  WILVLSGGISASLFTSTNNVNTTTCFEGFSKRVKTKITIFIEVVGFIPLILNVS 222
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QY      190  CSLKVVTALAQRPTDVGQAEAT-RKAARMVWALLVVFVCFPLHLVGLTVRLAVGWNA 248
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB      223  CSSVVLRTL--RKPAATLSQIGTNKKKVLKMITVHMAVVFVCFVPYNSVLFYALVRSQAI 280
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY      249  --ALLETIRRALY-ITSKLSDANCCLDAICYYYMAKEQESALAVAPRAKAHKSODSLC 305
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
DB      281  TNCFLERFAKIMYPITLCLATLNCPCDPFIYFTLESFQKSFYI-----NAHIRMESLF 334
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY      306  VT 307
      |
DB      335  KT 336

RESULT 9
US-10-042-211A-176
; Sequence 176, Application US/10042211A
; Publication No. US20030170719A1
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Akio et al.
; TITLE OF INVENTION: NFkB Activating Gene
; FILE REFERENCE: 1254-0192P
; CURRENT APPLICATION NUMBER: US/10/042,211A
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: JP 2000-402288
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 2001-088912
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-254018
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/278,640
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/314,385
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 176
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-211A-176

Query Match      24.9%; Score 402; DB 14; Length 370;
Best Local Similarity 34.1%; Pred. No. 6.3e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;
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Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;
QY 25 AVLGVLVLLGSLNLSALWVFCRMOQWTTETRIYMTNLAVADCLLCTLPF-VLHSLR-- 81
Db 44 AVYSVVFILGLTNSVLSVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNFNRH 103
QY 82 -DTSPTPLCOLSOGIYLTNRNYSISLVTAIAVDYVAVRHPRLRGLRSPROAAAVCAVL 140
Db 104 WPFQGT-LCKISGTAFLNIYGSMLFLTCISVDRELAIVYPRSRITRNRNSAIVCAGV 162
QY 141 WVLVIGSLVARWLLGIQE-----GGFCFRSTRHNFNSMR--FPLLGFYLPVAVVVF 189
Db 163 WILVLSGGISASLSFTTNVNNATTTCFEGFSKRVWKYLSKITIFIEVVGFIIPLILNVS 222
QY 190 CSLKVVTALAQRPPTDVQAEAT-RKAARMVWVANLLVFCPLPLHVLGTVRLAVGWNA 248
Db 223 CSSVVLRTL--RKPATLSQIGTNKKVKLMITVHMAVFCVFPVNSVLFVLYALVRSQAI 280
QY 249 --ALLETIRRALY-ITSKLSANCCDAICYYYMAKEQESALAVAPRAKAHKSODSLC 305
Db 281 TNCFLERFAKIMYPITLCLATLNCDFDPFIYYFTLESFQKSPYI-----NAHIRMESLF 334
QY 306 VT 307
Db 335 KT 336

RESULT 10
US-10-268-332-11
; Sequence 11, Application US/10268332
; Publication No. US2003017548A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY3, EXPRESSED HIGH
; FILE REFERENCE: D0042A CIP
; CURRENT APPLICATION NUMBER: US/10/268,332
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: U.S. 60/235,713
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: U.S. 60/261,783
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: U.S. 60/305,085
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: U.S. 60/313,171
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: U.S. 09/964,821
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 11
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-268-332-11

Query Match 24.9%; Score 402; DB 14; Length 370;
Best Local Similarity 34.1%; Pred. No. 6.3e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;
QY 25 AVLGVLVLLGSLNLSALWVFCRMOQWTTETRIYMTNLAVADCLLCTLPF-VLHSLR-- 81
Db 44 AVYSVVFILGLTNSVLSVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNFNRH 103
QY 82 -DTSPTPLCOLSOGIYLTNRNYSISLVTAIAVDYVAVRHPRLRGLRSPROAAAVCAVL 140
Db 104 WPFQGT-LCKISGTAFLNIYGSMLFLTCISVDRELAIVYPRSRITRNRNSAIVCAGV 162
QY 141 WVLVIGSLVARWLLGIQE-----GGFCFRSTRHNFNSMR--FPLLGFYLPVAVVVF 189
Db 163 WILVLSGGISASLSFTTNVNNATTTCFEGFSKRVWKYLSKITIFIEVVGFIIPLILNVS 222
QY 190 CSLKVVTALAQRPPTDVQAEAT-RKAARMVWVANLLVFCPLPLHVLGTVRLAVGWNA 248

Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;
QY 25 AVLGVLVLLGSLNLSALWVFCRMOQWTTETRIYMTNLAVADCLLCTLPF-VLHSLR-- 81
Db 44 AVYSVVFILGLTNSVLSVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNFNRH 103
QY 82 -DTSPTPLCOLSOGIYLTNRNYSISLVTAIAVDYVAVRHPRLRGLRSPROAAAVCAVL 140
Db 104 WPFQGT-LCKISGTAFLNIYGSMLFLTCISVDRELAIVYPRSRITRNRNSAIVCAGV 162
QY 141 WVLVIGSLVARWLLGIQE-----GGFCFRSTRHNFNSMR--FPLLGFYLPVAVVVF 189
Db 163 WILVLSGGISASLSFTTNVNNATTTCFEGFSKRVWKYLSKITIFIEVVGFIIPLILNVS 222
QY 190 CSLKVVTALAQRPPTDVQAEAT-RKAARMVWVANLLVFCPLPLHVLGTVRLAVGWNA 248
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Db 223 CSSVVLRTL--RKPATLSQIGTNKKVKLMITVHMAVFCVFPVNSVLFVLYALVRSQAI 280
QY 249 --ALLETIRRALY-ITSKLSANCCDAICYYYMAKEQESALAVAPRAKAHKSODSLC 305
Db 281 TNCFLERFAKIMYPITLCLATLNCDFDPFIYYFTLESFQKSPYI-----NAHIRMESLF 334
QY 306 VT 307
Db 335 KT 336

RESULT 11
US-10-617-217A-176
; Sequence 176, Application US/10617217A
; Publication No. US20040081986A1
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Akio et al.
; TITLE OF INVENTION: NF-kB ACTIVATING GENE
; FILE REFERENCE: 1254-0229P
; CURRENT APPLICATION NUMBER: US/10/617,217A
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: JP 2000-402288
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 2001-088912
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-254018
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/278,640
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/314,385
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 176
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-617-217A-176

Query Match 24.9%; Score 402; DB 15; Length 370;
Best Local Similarity 34.1%; Pred. No. 6.3e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;
QY 25 AVLGVLVLLGSLNLSALWVFCRMOQWTTETRIYMTNLAVADCLLCTLPF-VLHSLR-- 81
Db 44 AVYSVVFILGLTNSVLSVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNFNRH 103
QY 82 -DTSPTPLCOLSOGIYLTNRNYSISLVTAIAVDYVAVRHPRLRGLRSPROAAAVCAVL 140
Db 104 WPFQGT-LCKISGTAFLNIYGSMLFLTCISVDRELAIVYPRSRITRNRNSAIVCAGV 162
QY 141 WVLVIGSLVARWLLGIQE-----GGFCFRSTRHNFNSMR--FPLLGFYLPVAVVVF 189
Db 163 WILVLSGGISASLSFTTNVNNATTTCFEGFSKRVWKYLSKITIFIEVVGFIIPLILNVS 222
QY 190 CSLKVVTALAQRPPTDVQAEAT-RKAARMVWVANLLVFCPLPLHVLGTVRLAVGWNA 248
Db 223 CSSVVLRTL--RKPATLSQIGTNKKVKLMITVHMAVFCVFPVNSVLFVLYALVRSQAI 280
QY 249 --ALLETIRRALY-ITSKLSANCCDAICYYYMAKEQESALAVAPRAKAHKSODSLC 305
Db 281 TNCFLERFAKIMYPITLCLATLNCDFDPFIYYFTLESFQKSPYI-----NAHIRMESLF 334
QY 306 VT 307
Db 335 KT 336

RESULT 12
US-10-753-267-86
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; Sequence 86, Application US/10753267
; Publication No. US20050037946A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Stagliano, Nancy E.
; APPLICANT: Healy, Aileen L.
; APPLICANT: Acton, Susan L.
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Donoghue, Mary A.
; APPLICANT: Rodrique-Way, Amelie
; APPLICANT: Tomlinson, James E.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1722, 10280, 59917, 85553,
; TITLE OF INVENTION: 10653, 9235, 21668, 17794, 2210, 6169, 10102, 21061, 17662,
; TITLE OF INVENTION: 1468, 12282, 6350, 9035, 1820, 23652, 7301, 8925, 8701,
; TITLE OF INVENTION: 3533, 9462, 9123, 12788, 17729, 65552, 1261, 21476, 33770,
; TITLE OF INVENTION: 9380, 2569654, 33556, 53656, 44143, 32612, 10671, 261,
; TITLE OF INVENTION: 44570, 41922, 2552, 2417, 19319, 43969, 8921, 8993, 955,
; TITLE OF INVENTION: 3245, 966, 1920, 17318, 1510, 14180, 26005, 554, 16408,
; TITLE OF INVENTION: 42028, 112091, 13886, 13942, 1673, 54946 OR 2419
; FILE REFERENCE: MPI03-003PRNOMNTM
; CURRENT APPLICATION NUMBER: US/10/753,267
; CURRENT FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: US 60/439,683
; PRIOR FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US 60/445,216
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/448,036
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: US 60/454,189
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/457,541
; PRIOR FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: US 60/466,411
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: US 60/469,041
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/477,414
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: US 60/478,560
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/489,772
; PRIOR FILING DATE: 2003-07-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-753-267-86

Query Match 24.9%; Score 402; DB 17; Length 370;
Best Local Similarity 34.1%; Pred. No. 6.3e-30;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

Qy 25 AYLGVLVLGLLNSLALWFCRCMQQWETRTYMTNLAVADICLLCTLPF-VLHSLR-- 81
Db 44 AVTSVVFILGLITNSVLSFVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYFNHRH 103

Qy 82 -DTSDTPLCQSQIYLTNRYSISLVTAIVADRYVAVRHLRARGLSRPRQAAAVCAVL 140
Db 104 WPFQDT-LCKISGTAFTNIYGSMLFLTICISVDRLAIVYVFRSRTIRTRNSAIVCAGV 162

Qy 141 WLVIGSLVARWLLGTOE-----GGCFRSTRHNFNSMR--FPLLGFYLPVAVVF 189
Db 163 WILVLSGGISASLSFTTNVNNATTCTCEGFSKRVKTKYLSKITIFIEVVGFIILNVS 222

Qy 190 CSLKVVYALQRPPTDVQAEAT-RKAARVMWANLLVVFVCFPLPLHVGTLVLAGWNA 248
Db 223 CSSVVLRTL--RKPATLSQIGTNKKVVKMTVTHMAVVFVFCFVYNSVLFYALVRSQAI 280

Qy 249 --ALLETIRRALY-ITSKLSDANCCCLDAICYYYMAKEFOEASALAVAPRAKAH 305
; Sequence 10, Application US/09964821B
; Publication No. US20030186360A1
; GENERAL INFORMATION:
; APPLICANT: FEDER, J. N.
; APPLICANT: MINTIER, G.
; APPLICANT: RAMANATHAN, C. S.
; APPLICANT: HAWKEN, D.R.
; APPLICANT: CACACE, A.
; APPLICANT: BARBER, L.
; APPLICANT: KORNACKER, M. G.
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMV3,
; TITLE OF INVENTION: EXPRESSED HIGHLY IN IMMUNE- AND COLON- RELATED TISSUES
; FILE REFERENCE: D0042NP
; CURRENT APPLICATION NUMBER: US/09/964,821B
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/235,713
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/261,783
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/305,085
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/313,171
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 370
; TYPE: PRT
; ORGANISM: HUMAN
US-09-964-821B-10

Query Match 24.8%; Score 401; DB 10; Length 370;
Best Local Similarity 34.0%; Pred. No. 7.9e-30;
Matches 105; Conservative 58; Mismatches 104; Indels 42; Gaps 11

Qy 25 AYLGVLVLGLLNSLALWFCRCMQQWETRTYMTNLAVADICLLCTLPF-VLHSLR-- 81
Db 44 AVTSVVFILGLITNSVLSFVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYFNHRH 103

Qy 82 -DTSDTPLCQSQIYLTNRYSISLVTAIVADRYVAVRHLRARGLSRPRQAAAVCAVL 140
Db 104 WPFQDT-LCKISGTAFTNIYGSMLFLTICISVDRLAIVYVFRSRTIRTRNSAIVCAGV 162

Qy 141 WLVIGSLVARWLLGTOEGF-----CFR-----STRHNFNSMRPPLGFLYL 182
Db 163 WILVLSG-----GISASLSFTTNVNNATTCTCEGLSKRVKTKYLSKITIFIEVVGFI 215

Qy 183 PLAVVYFCSLKVVYALQRPPTDVQAEAT-RKAARVMWANLLVVFVCFPLPLHVGTLVRL 241
Db 216 PLILNVSCSSVVLRTL--RKPATLSQIGTNKKVVKMTVTHMAVVFVFCFVYNSVLFYLA 273

Qy 242 AVGWNAC--ALLETIRRALY-ITSKLSDANCCCLDAICYYYMAKEFOEASALAVAPRAKAH 298
Db 274 LVRSQAITNCFLERFKIMYPITLCATLNCCTDPPIFYITLESFQKSFVI-----NAH 327

Qy 299 KSQDSLQVT 307
Db 328 IRMESLFKT 336

RESULT 14
US-10-268-332-10
; Sequence 10, Application US/10268332

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; Publication No. US20030175748A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY3, EXPRESSED HIGHLY
; FILE REFERENCE: D0042A CIP
; CURRENT APPLICATION NUMBER: US/10/268,332
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: U.S. 60/235,713
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: U.S. 60/261,783
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: U.S. 60/305,085
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: U.S. 60/313,171
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: U.S. 09/964,821
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-268-332-10

Query Match      24.8%; Score 401; DB 14; Length 370;
Best Local Similarity 34.0%; Pred. No. 7.9e-30;
Matches 105; Conservative 58; Mismatches 104; Indels 42; Gaps 11;

Qy      25  AYLGVLLVLGLLNSLALWVFCRQMQWTETRIYMTNLAVADLCLLTLPF-VLHSLR-- 81
Db      44  AVYSVVFILGLITNSASLVFCFRMKRSETATFITNLAVSDLLFVCTLPFKIFYNFRH 103

Qy      82  -DTSPTPLCQLSQGIYLTNRNYSISLVTAIAVDRYVAVRHPRLRAGLSRPROAAVCAVL 140
Db      104  WPFQGT-LCKISGTAFLTNIYGSMLFLTCISVDRLAIVPFRSRTIIRNSAIVCAGV 162

Qy      141  WVLVIGSIVARWLLGIQEGF-----CFR-----STRHNFNSMRFPPLLGFYL 182
Db      163  WILVLSG-----GISASLSTNNVNNATTCFGLSKRVWKTYLSKITIFIEVVGFI 215

Qy      183  PLAVVFCSLKVVTALAQRPTDVQAEAT-RKAARMVWANLLVFVVCFLPLHVLGLTVRL 241
Db      216  PLILNVSCSVVLRTL--RKPATLSQIGTNKKVKLKMIVHMAVFCVFPVNSVLFLYA 273

Qy      242  AVGNWAC--ALLETRRALLY-ITSKLSDANCLDAICYVMKAEQASALAVAPRAK 298
Db      274  LVRQAITNCFERFAKIMYRITLCLATLNCDFDPFIYYFTLESFQSFYI-----NAH 327

Qy      299  KSQDSLQCVT 307
Db      328  IRMESLFT 336

RESULT 15
US-10-024-298A-174
; Sequence 174, Application US/10024298A
; Publication No. US20030143540A1
; GENERAL INFORMATION:
; APPLICANT: ASAHI KASEI KABUSHIKI KAISHA
; APPLICANT: AKIO MATSUDA
; APPLICANT: GOICHI HONDA
; APPLICANT: SHUJI MURAMATSU
; APPLICANT: YUKIKO NAGANO
; TITLE OF INVENTION: NF-K B Activating Gene
; FILE REFERENCE: 1254-0191P
; CURRENT APPLICATION NUMBER: US/10/024,298A
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/314,385
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/278,641
; PRIOR FILING DATE: 2001-03-26

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; PRIOR APPLICATION NUMBER: 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP254018/2001
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: JP0088912/2001
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP402288/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 174
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-024-298A-174

Query Match      24.3%; Score 392; DB 14; Length 370;
Best Local Similarity 34.5%; Pred. No. 5.7e-29;
Matches 97; Conservative 58; Mismatches 104; Indels 22; Gaps 9;

Qy      25  AYLGVLLVLGLLNSLALWVFCRQMQWTETRIYMTNLAVADLCLLTLPF-VLHSLR-- 81
Db      44  AVYSVVFILGLITNSASLVFCFRMKRSETATFITNLALSDLLFVCTLPFKIFYNFRH 103

Qy      82  -DTSPTPLCQLSQGIYLTNRNYSISLVTAIAVDRYVAVRHPRLRAGLSRPROAAVCAVL 140
Db      104  WPFQGT-LCKISGTAFLTNIYGSMLFLTCISVDRLAIVPFRSRTIIRNSAIVCAGV 162

Qy      141  WVLVIGSIVARWLLGIQEGF-----GGFCFRSTRHNFNSMR--FPLLGFYLPVAVVVF 189
Db      163  WILVLSGGISASLSTNNVNNATTCFGLSKRVWKTYLSKITIFIEVVGFIPLILNV 222

Qy      190  CSLKVVTALAQRPTDVQAEAT-RKAARMVWANLLVFVVCFLPLHVLGLTVRLAYGNAC 248
Db      223  CSSVVLRTL--RKPATLSQIGTNKKVKLKMIVHMAVFCVFPVNSVLFYALVRSQAI 280

Qy      249  --ALLETRRALLY-ITSKLSDANCLDAICYVMKAEQEA 286
Db      281  TNCLLERFAKIMYRITLCLATLNCDFDPFIYYFTLESFQKS 321

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Job time : 56 secs

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GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: May 23, 2005, 11:09:25 ; Search time 58.5 Seconds  
(without alignments)  
2704.829 Million cell updates/sec

Title: US-10-083-168-85  
Perfect score: 1615  
Sequence: 1 MNGTYNTCGSSDLTWPPAIK.....AVAPRAKHKQSDSLCVTLA 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Query	ID	Description
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2	1597	98.9	394	2 Q6ZMP9	Q6zmp9 homo sapien
3	1123	69.5	307	1 GP35 MOUSE	Q9es90 mus musculus
4	1122	69.5	307	2 Q8CB97	Q8cb97 mus musculus
5	1108	68.6	307	2 Q8BS98	Q8bs98 mus musculus
6	401	24.8	370	1 P2Y9 HUMAN	Q99677 homo sapien
7	399	24.7	370	2 Q6NSP5	Q6nsp5 homo sapien
8	399	24.7	370	2 Q8BKK1	Q8bkk1 mus musculus
9	391	24.2	370	2 Q8BLG2	Q8blg2 mus musculus
10	376.5	23.3	363	2 Q8TDS4	Q8tds4 homo sapien
11	374	23.2	319	2 Q8N580	Q8n580 homo sapien
12	369.5	22.9	387	1 G09B HUMAN	P49019 homo sapien
13	369.5	22.9	387	2 Q8NGE4	Q8nge4 homo sapien
14	367.5	22.8	308	1 P2Y5 CHICK	P32250 gallus gall
15	366	22.7	347	2 Q7ZAA4	Q7zza4 brachydanio
16	360.5	22.3	296	2 Q9WU09	Q9wu09 rattus norv
17	360.5	22.3	344	1 P2Y5 HUMAN	P43657 homo sapien
18	360.5	22.3	344	2 Q7Z3S0	Q7z3s0 homo sapien
19	360.5	22.3	344	2 Q7Z3S6	Q7z3s6 homo sapien
20	360	22.3	372	1 GP92 HUMAN	Q8hlc0 homo sapien
21	356.5	22.1	344	1 P2Y5 MOUSE	Q8bmc0 mus musculus
22	348.5	21.6	360	2 Q9EP66	Q9ep66 mus musculus
23	338	20.9	319	2 Q9Y2T6	Q9y2t6 homo sapien
24	337.5	20.9	360	2 Q80Z39	Q80z39 rattus norv
25	330	20.4	298	2 Q8VE54	Q8ve54 mus musculus
26	329.5	20.4	374	1 P2Y2 RAT	P41232 rattus norv
27	328.5	20.3	377	1 P2Y2 HUMAN	P41321 homo sapien
28	326	20.2	346	1 GP81 HUMAN	Q9bxc0 homo sapien
29	321.5	19.9	345	1 CLT2_PIG	Q95n03 sus scrofa
30	320	19.8	349	2 Q6P852	Q6p852 xenopus tro
31	319.5	19.8	343	1 GP81_MOUSE	Q8c131 mus musculus

32	319.5	19.8	361	1 P2Y4 RAT	O35811 rattus norv
33	319	19.8	346	2 Q6NXU5	Q6nxu5 homo sapien
34	317	19.6	373	1 P2Y2 MOUSE	P35383 mus musculus
35	316.5	19.6	346	1 CLT2 HUMAN	Q9n875 homo sapien
36	316	19.6	309	1 CLT2 RAT	Q924t9 rattus norv
37	316	19.6	362	1 P2YR_CHICK	P34996 gallus gall
38	316	19.6	362	1 P2YR_MELGA	P49652 meleagris g
39	316	19.6	374	2 O57466	O57466 meleagris g
40	315.5	19.5	365	1 P2Y4 HUMAN	P51582 homo sapien
41	314.5	19.5	361	1 P2Y4 MOUSE	Q9j1s7 mus musculus
42	314.5	19.5	396	1 BRB2 RAT	P25023 rattus norv
43	314	19.4	328	1 P2Y6 RAT	Q63371 rattus norv
44	311.5	19.3	362	1 GP84_HUMAN	P46093 homo sapien
45	311.5	19.3	362	2 Q6NWM4	Q6nwm4 homo sapien

#### ALIGNMENTS

#### RESULT 1

ID	GP35_HUMAN	STANDARD;	PRT;	309 AA.
AC	Q9HC97; O43495; Q86UH4;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	29-MAR-2004 (Rel. 43, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Probable G protein-coupled receptor GPR35.			
GN	Name=GPR35;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98140132; PubMed=9479505; DOI=10.1006/geno.1998.5095;			
RA	O'Dowd B.F., Nguyen T., Marchese A., Cheng R., Lynch K.R.,			
RA	Heng H.H.Q., Kolakowski L.F. Jr., George S.R.;			
RT	"Discovery of three novel G-protein-coupled receptor genes."			
RL	Genomics 47:310-313(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A., AND VARIANTS THR-25; ILE-29; MET-108; SER-125;			
RP	MET-253 AND SER-294.			
RX	MEDLINE=20472315; PubMed=11017071; DOI=10.1038/79876;			
RA	Horikawa Y., Oda N., Cox N.J., Li X., Orho-Melander M., Hara M.,			
RA	Hinokio Y., Lindner T.H., Mashima H., Schwarz P.E.H.,			
RA	del Bosque-Plata L., Horikawa Y., Oda Y., Yoshiuchi I., Colilla S.,			
RA	Polonsky K.S., Wei S., Concannon P., Iwasaki N., Schulze J.,			
RA	Baier L.J., Bogardus C., Groop L., Boerwinkle E., Hanis C.L.,			
RA	Bell G.I.;			
RT	"Genetic variation in the gene encoding calpain-10 is associated with			
RT	type 2 diabetes mellitus."			
RL	Nat. Genet. 26:163-175(2000).			
RN	[3]			
RP	SEQUENCE FROM N.A., AND VARIANT SER-294.			
RA	Warren C.N., Aronstam R.S., Sharma S.V.;			
RT	"cDNA clones of human proteins involved in signal transduction			
RT	sequenced by the Guthrie cDNA resource center (www.cdna.org).";			
RT	Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: Orphan receptor			
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).			
CC	-!- TISSUE SPECIFICITY: Expressed in all adult and fetal tissues			
CC	examined, including pancreatic islets and skeletal muscle, with			
CC	relatively higher levels in adult lung, small intestine, colon and			
CC	stomach.			
CC	-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch)			



DE Probable G protein-coupled receptor GPR35.  
GN Name=Gpr35;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
RX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20472315; PubMed=11017071; DOI=10.1038/79876;  
RA Horikawa Y., Oda N., Cox N.J., Li X., Orho-Melander M., Hara M.,  
RA Hinokio Y., Lindner T.H., Mashima H., Schwarz P.E.H.,  
RA del Bosque-Plata L., Horikawa Y., Oda Y., Yoshiuchi I., Colilla S.,  
RA Polonsky K.S., Wei S., Concannon P., Iwasaki N., Schulze J.,  
RA Baier L.J., Bogardus C., Groop L., Boerwinkle E., Hanis C.L.,  
RA Bell G.I.;  
RT "Genetic variation in the gene encoding calpain-10 is associated with  
RT type 2 diabetes mellitus.";  
RL Nat. Genet. 26:163-175(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX STRAIN=C57BL/6J; TISSUE=Mammary gland;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh F.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Roak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: Orphan receptor.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AF200349; AAH18487.1; -;  
DR EMBL; BC027429; AAG27429.1; -;  
DR MGD; MGI:1929509; Gpr35.  
DR InterPro; IPR000276; GPCR Rhodopsn.  
DR InterPro; IPR002286; P2\_purnoceptor.  
DR Pfam; PF00001; 7tm1; 1.  
DR PRINTS; PR00237; GPCRHHODPSN.  
DR PROSITE; PS00237; G PROTEIN RECEPTOR F1\_1; 1.  
DR PROSITE; PS0262; G PROTEIN RECEPTOR F1\_2; 1.  
KW G-protein coupled receptor; Glycoprotein; Transmembrane.  
FT DOMAIN 1 18 Extracellular (Potential).  
FT TRANSMEM 19 39 1 (Potential).  
FT DOMAIN 40 53 Cytoplasmic (Potential).  
FT TRANSMEM 54 74 2 (Potential).  
FT DOMAIN 75 88 Extracellular (Potential).  
FT TRANSMEM 89 110 3 (Potential).  
FT DOMAIN 111 129 Cytoplasmic (Potential).  
FT TRANSMEM 130 150 4 (Potential).  
FT DOMAIN 151 176 Extracellular (Potential).

FT TRANSMEM 177 197 5 (Potential).  
FT DOMAIN 198 217 Cytoplasmic (Potential).  
FT TRANSMEM 218 238 6 (Potential).  
FT DOMAIN 239 257 Extracellular (Potential).  
FT TRANSMEM 258 278 7 (Potential).  
FT DOMAIN 279 307 Cytoplasmic (Potential).  
FT DISULFID 87 160 By similarity.  
FT CARBOHYD 2 2 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 7 7 N-linked (GlcNAc...) (Potential).  
SQ SEQUENCE 307 AA; 34151 MW; 0B3D02CECB16710D CRC64;  
Query Match 69.5%; Score 1123; DB 1; Length 307;  
Best Local Similarity 71.9%; Pred. No. 5.3e-76;  
Matches 223; Conservative 30; Mismatches 51; Indels 6; Gaps 5;  
QY 1 MNGTYNTCGSSDLTPPAIKLGFYAYLGLVLLGLLLNSLALWVFCRCMQQTETRIYMT 60  
DB 1 MNST--TCNST-LTWPAVSNVNFIIYSALLVLLGLLLNSVALWVFCYRHMOWTETRIYMT 57  
QY 61 NLAVADLCCLCTLPFVLSLR-DTSDFLCQLSQIYLTNRYSISLVTAIAVDYVAVR 119  
DB 58 NLAVADLCCLCSLPFVLSLYSSSDTFVCSQIYLTNRYSISLVTAIAVDYVAVR 117  
QY 120 HPLRARGLRSPQAAAVCAVLWLVIGSLVARWLLGIQGGFCFS-TRHNFSNMFPL 178  
DB 118 HPLRARELRSPQAAAVCAVLWLVVITSLVVRWRLGMQEGGFCFSQTRNFSSTAFSL 177  
QY 179 GFYPLAVVVFCSLKVVTALAQRPPTDVQGAETRAKRWVWVWVWVWVWVWVWVWVWV 238  
DB 178 GFYPLAVVVFCSLKVVTALVSRPAADVQGAETRAKRWVWVWVWVWVWVWVWVWV 237  
QY 239 VRLAVGWV 298  
DB 238 VQVSLNLTCAARDTFSRSLSTGKLSITGKLSITGKLSITGKLSITGKLSITGKLSIT 296  
QY 299 KSQSLCVTL 308  
DB 297 KSQSLCVTL 306  
RESULT 4  
QSCB97 PRELIMINARY; PRT; 307 AA.  
AC Q8CB97  
ID Q8CB97;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Mus musculus adult male bone cDNA, RIKEN full-length enriched library,  
DE clone:9830121M19 product:G protein-coupled receptor 35, full insert  
DE sequence.  
GN Name=Gpr35;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RX SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Bone;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44(1999).  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=C57BL/6J; TISSUE=Bone;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Bone;  
RA RIKEN FANTOM Consortium;  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Bone;  
RA RIKEN FANTOM Consortium;





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RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RC TISSUE=Embryonic body between diaphragm region and neck;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Haneagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka I.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AK034870; BAC28861.1; -.
DR MGI; 1929509; Gpr35.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR002286; P2_purnocptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PRINTS; PR01157; P2PURNOCPT.
DR PROSITE; PS00237; G-PROTEIN RECF_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECF_F1_2; 1.
DR G-protein coupled receptor; Transmembrane.
KW SEQUENCE 307 AA; 34260 MW; 923D02CECB0D70AC CRC64;
Query Match 68.6%; Score 1108; DB 2; Length 307;
Best Local Similarity 71.3%; Pred. No. 6.9e-75;
Matches 221; Conservative 30; Mismatches 53; Indels 6; Gaps 5;
Qy 1 MNGVTNCGSDLTWPPAIIKLGFAVLGVLLVGLLLSLALWVFCRMQWTERIYWT 60
Db 1 MNST--TCNST-LTPASVNNFFIYISALLLVGLLLSVLWVFCYRHWQTERIYWT 57
Qy 61 NLAVALDCLLCTLPVFLHSLR-DTSDTPLCOLSQGIYLTNRNYSLSLVTALAVDRYAVR 119
Db 58 NLAVALDCLLCSLPVFLSLKYSSTDPVCSLSQGIYLANRYSLSLVTALAVDRYAVR 117
Qy 120 HPLRARGLRSPQAAAVCAVLVVLVIGSLVAVRLVGLIQQGFCPRS-TRHNFNSMRPFL 178
Db 118 HPLRARELRSPQAAAVCAVLVVLVTVSLVVRWRLGMOEGGFCFSSTTRNPFSTTAFSLL 177
Qy 179 GFYLPVAVVFCSLKVVVTLAQRPTDVGQAEATKAKRWVWVWVWVWVWVWVWVWVWVWV 238
Db 178 GFYLPVAVVFCSLQVTVLVRPAADVGQAEATKQTHWVWVWVWVWVWVWVWVWVWVWV 237
Qy 239 VRLAVGNACALLETIRRALYITSLKSDANCLDAICVYYMAKEFOEASALAVAPRAKH 298
Db 238 VQVSLNLTCAARDTFSRSLITGKLSDTNCLDAICVYYMAKEFOEAFKPTSNT-PH 296
Qy 299 KSQDSLCLVTL 308
Db 297 KSQYSQILSL 306
RESULT 6
ID P2Y9 HUMAN STANDARD; PRT; 370 AA.
AC Q99677; O15112;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE P2Y purinoceptor 9 (p2y9); (Purinerigic receptor 9) (G protein-coupled

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DE receptor GPR23) (P2Y5-like receptor).
GN Name=GPR23; Synonym=P2RY9;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97225799; PubMed=9073069; DOI=10.1016/S0378-1119(96)00722-6;
RA O'Dowd B.F., Nguyen T., Jung B.P., Marchese A., Cheng R., Heng H.H.Q.,
RT Kolakowski L.F. Jr., Lynch K.R., George S.R.;
RT "Cloning and chromosomal mapping of four putative novel human G-
RT protein-coupled receptor genes.";
RL Gene 187:75-81(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Bohm S.K., Khitin L.M., Payan D.P., Bunnett N.W.;
RN Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97366605; PubMed=9223435; DOI=10.1006/bbr.1997.6895;
RA Janssens R., Boeynaems J.M., Godart M., Communi D.;
RT "Cloning of a human heptahelical receptor closely related to the P2Y5
RT receptor.";
RL Biochem. Biophys. Res. Commun. 236:106-112(1997).
RN [4]
RP SEQUENCE FROM N.A.
RA Kopatz S.A., Aronstam R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Bird C.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Not detected in the brain regions thalamus,
CC putamen, caudate, frontal cortex, pons, hypothalamus and
CC hippocampus.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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CC or send an email to license@isb-sib.ch).
DR EMBL; U66578; AAC51301.1; -.
DR EMBL; U90323; AAB62087.1; -.
DR EMBL; U90322; AAB62088.1; -.
DR EMBL; AF005419; AAB66322.1; -.
DR EMBL; AY301274; AAP58404.1; -.
DR EMBL; AL590083; CAD18851.1; -.
DR HSSP; P34996; 1DDD.
DR Genes; HGNC:4478; GPR23.
DR MIM; 300086; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.
DR InterPro; IPR00276; GPCR_Rhodpsn.
DR InterPro; IPR002188; P2Y5_purnocptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G-PROTEIN RECF_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECF_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT DOMAIN 1 43 Extracellular (Potential).
FT TRANSMEM 44 64 1 (Potential).
FT DOMAIN 65 73 Cytoplasmic (Potential).
FT TRANSMEM 74 94 2 (Potential).

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FT DOMAIN          95 112 Extracellular (Potential).
FT TRANSMEM       113 133 3 (Potential).
FT DOMAIN         134 155 Cytoplasmic (Potential).
FT TRANSMEM       156 176 4 (Potential).
FT DOMAIN         177 203 Extracellular (Potential).
FT TRANSMEM       204 224 5 (Potential).
FT DOMAIN         225 254 Cytoplasmic (Potential).
FT TRANSMEM       255 275 6 (Potential).
FT DOMAIN         276 294 Extracellular (Potential).
FT TRANSMEM       295 315 7 (Potential).
FT DOMAIN         316 370 Cytoplasmic (Potential).
FT DISULFID       111 188 By similarity.
FT CARBOHYD       15 15 N-linked (GlcNAc...) (Potential).
FT CARBOHYD       24 24 N-linked (GlcNAc...) (Potential).
FT CARBOHYD       28 28 N-linked (GlcNAc...) (Potential).
FT CARBOHYD       183 183 N-linked (GlcNAc...) (Potential).
FT CONFLICT       192 192 F -> L (in Ref. 3).
SQ SEQUENCE       370 AA; 41895 MW; 20857F52A3929E48 CRC64;

Query Match          24.8%; Score 401; DB 1; Length 370;
Best Local Similarity 34.1%; Pred. No. 4.5e-22;
Matches 103; Conservative 60; Mismatches 111; Indels 28; Gaps 10;

QY 25 AYLVLLVGLLNSLALWVFCRQMQWTEIRYMTNLAVADLCCLCTLPF-VLHSLR-- 81
DB 44 AVYSVVFILGILTNSVSLFVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNRHH 103

QY 82 -DTSPTPLCOLSQGQIYLTNRYSISLVTAIAVDVAVRHPLRAGLRSPROAAVCAVL 140
DB 104 WPFQGT-LCKISGTAFLNIYGSMLFLTCISVDRLAIVYPRSTIRTRNSAIVCAGV 162

QY 141 WVLVIGSLVARWLLGIOE-----GGFCFRSTRHNFNSMR--FPLLGFYLPLAVVVF 189
DB 163 WILVLSGGISASLFTSTNNVNTTCFEGFSKRVKMTYLSKITIFIEVVGFIPLILNVS 222

QY 190 CSLKVVVTAALQRPPTDVQAEAT-RKAKRWVWVWVVCFLPLHVLGTVRLAVGMNAC 248
DB 223 CSSVVLRTL--RKPAFLSQIGTKNKKVLMITHVMAVFCVFPVNSVLFYALVRSQAI 280

QY 249 --ALLETIRRALY-ITSKLSDANCCDAICYYIMAKFQEASALAVAPRAKAKHSQDSL 305
DB 281 TNCFLERFAKIMYPITLCLATLNCDFPFYFYFTLESFQKSPYI-----NAHIRMESL 334

QY 306 VT 307
DB 335 KT 336

RESULT 7
Q6NSP5 PRELIMINARY; PRT; 370 AA.
AC Q6NSP5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE G protein-coupled receptor 23.
GN Name=GPR23;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hulyk S.W.,
RA Fahney J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RA Strausberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC069996; AAH69996.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045028; F:purinergic nucleotide receptor activity; G- . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR002188; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1.1.
DR PRINTS; PR00237; GPCR_Rhodpsn.
DR PRINTS; PR01067; P2Y5ORPHANR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 370 AA; 41867 MW; 2AB4B3F5F43FF83 CRC64;

Query Match          24.7%; Score 399; DB 2; Length 370;
Best Local Similarity 34.1%; Pred. No. 6.3e-22;
Matches 103; Conservative 59; Mismatches 112; Indels 28; Gaps 10;

QY 25 AYLVLLVGLLNSLALWVFCRQMQWTEIRYMTNLAVADLCCLCTLPF-VLHSLR-- 81
DB 44 AVYSVVFILGILTNSVSLFVFCFRMKRSETAIFITNLAVSDLLFVCTLPFKIFYNRHH 103

QY 82 -DTSPTPLCOLSQGQIYLTNRYSISLVTAIAVDVAVRHPLRAGLRSPROAAVCAVL 140
DB 104 WPFQGT-LCKISGTAFLNIYGSMLFLTCISVDRLAIVYPRSTIRTRNSAIVCAGV 162

QY 141 WVLVIGSLVARWLLGIOE-----GGFCFRSTRHNFNSMR--FPLLGFYLPLAVVVF 189
DB 163 WILVLSGGISASLFTSTNNVNTTCFEGFSKRVKMTYLSKITIFIEVVGFIPLILNVS 222

QY 190 CSLKVVVTAALQRPPTDVQAEAT-RKAKRWVWVWVVCFLPLHVLGTVRLAVGMNAC 248
DB 223 CSSVVLRTL--RKPAFLSQIGTKNKKVLMITHVMAVFCVFPVNSVLFYALVRSQAI 280

QY 249 --ALLETIRRALY-ITSKLSDANCCDAICYYIMAKFQEASALAVAPRAKAKHSQDSL 305
DB 281 TNCFLERFAKIMYPITLCLATLNCDFPFYFYFTLESFQKSPYI-----NAHIRMESL 334

QY 306 VT 307
DB 335 KT 336

RESULT 8
Q6BKK1 PRELIMINARY; PRT; 370 AA.
AC Q6BKK1;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length
DE 'enriched library, clone: D130067B12 product: P2Y PURINOCEPTOR 9, full
DE insert sequence.
GN Name=Gpr23;

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QY 142 VLVIGSLV--ARWLLGIEGG--FCFR--STRHNF--NSMRPPLIGFYPLPLAVVPCSLKV 194  
 Db 153 GITITGLVHLLKKMPVINGGGLNLCSSFSICHTFQWHEAMP--LLEFFFLGLGILFCSARI 211  
 QY 195 VTLAQRPTDVGQAEATKAKR---MYWANLVFVVCFLPLHVLGLTVRLAVGM----- 245  
 Db 212 IWSLQR-----QMDRAKIKRAITFMVAIVEVICFLP---SVVVRIRIFWLLHTSG 262  
 QY 246 -NACALLETIRRALYITSKLSDANCCLDCAICYNNAKEF 283  
 Db 263 TQNCVEVRSVDLAFITILSFTYMSMLDPVVVYFSSPSF 301

RESULT 11  
 QN580  
 ID QN580 PRELIMINARY; PRT; 319 AA.  
 AC QN580;  
 DT 01-OCT-2002 (TReMBLrel. 22, Created)  
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)  
 DE G protein-coupled receptor 55 (GPR55 protein) (Fragment).  
 GN Name=GPR55;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Pancreas;  
 RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,  
 RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Pancreas;  
 RA Strausberg R.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,  
 RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,  
 RA Korn B., Zuo D., Hu Y., Labaer J.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
 DR EMBL; BC032694; AAH32694.1; -  
 DR EMBL; CR541776; CAG46575.1; -  
 DR Genew; HGNC:4511; GPR55.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor protein activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.

DR PROSITE; PS00237; G\_PROTEIN\_RECP\_F1\_1; 1.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECP\_F1\_2; 1.  
 KW G-protein coupled receptor; Receptor; Transmembrane.  
 SQ SEQUENCE 319 AA; 36637 MW; D6E5C6CA8426E7D5 CRC64;

Query Match 23.2%; Score 374; DB 2; Length 319;  
 Best Local Similarity 35.5%; Pred. No. 4.1e-20;  
 Matches 98; Conservative 49; Mismatches 95; Indels 34; Gaps 10;

QY 32 VLGLLNSLALWVFC-----RMQWTEITRIYMTNLAVADLCILCTLPFLVLSLRDTSPT 87  
 Db 32 VLGLLNSLALWVFC-----RMQWTEITRIYMTNLAVADLCILCTLPFLVLSLRDTSPT 87  
 QY 88 -LCQLSQGIYLTNRYMSISLVTAIAVDYVAVRPLRAGLRSPQAAVCAVILVIV-I 145  
 Db 92 SLCTLVECLYFVSMYGSVFTTICFISMDRFLAIRVPLLVLSHLRSPRKIFGICCTIWLVT 151  
 QY 146 GSLVARMLGIGEGGFCFRSTRHNF-----SMRFLP--LGFYPLAVVVCSLKVVT 197  
 Db 152 GSIIPIYSFHGKVKYKMF-----HNSDDTWAKVFFPLEVFGFLDPMGIMFGCCSRSIH 207  
 QY 198 LAQRPTDVGQAEATR---KAKRWVW---ANLLVFWVCFLPLHVLGLTVRLAVGMW---AC 248  
 Db 208 L-----LGRDHTQDWVQKACIYISIAASLAVFVWSFLPVHLGFFLQFLVRNSFIVEC 260  
 QY 249 ALLETIRRALYITSKLSDANCCLDCAICYNNAKSFQ 284  
 Db 261 RAKQISIFFLQLSMCFSNVNCCLDVFCYFVFKRFR 296

RESULT 12  
 G09B HUMAN  
 ID G09B HUMAN STANDARD; PRT; 387 AA.  
 AC P49019;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Probable G protein-coupled receptor GPR109B (G protein-coupled  
 receptor HM74).  
 GN Name=GPR109B; Synonyms=HM74;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Monocytes;  
 RX MEDLINE=94092629; PubMed=7505609;  
 RA Nomura H., Nielsen B.W., Matsushima K.;  
 RT "Molecular cloning of cDNAs encoding a LD78 receptor and putative  
 leukocyte chemotactic peptide receptors.";  
 RL Int. Immunol. 5:1239-1249 (1993).  
 CC -!- FUNCTION: Orphan receptor.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 DR EMBL; D10923; BAA01721.1; -  
 DR FIR; I69202; I69202.  
 DR HSSP; P34996; 1DDD.  
 DR Genew; HGNC:16824; GPR109B.  
 DR MIM; 606039; -  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.







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